

A; Introns: 183/1; 247/1; 288/1; 318/1; 364/1; 388/2; 457/1; 481/2; 521/3
 Query Match Score 118; DB 2; Length 561;
 Best Local Similarity 36.8%; Pred. No. 0.00024;
 Matches 21; Conservative 11; Mismatches 23; Indels 2; Gaps 2;

Qy 12 CPSNEIFSRCDGRC-QRFCPNVPKPLCIKICAPGCVCRUGYLRNKKVYPRSKC 66
 Db 123 CPVNEVSNECHNPCTEKCPKNAPOVNCLMACQVGSCMDGFVRNNQGVCKEAC 179

RESULT 3
 Hypothetical protein Y69H2.3b - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 # sequence_revision 15-Oct-1999 # text_change 15-Oct-1999
 C; Accession: T27319
 R; McMurray, A.
 Submitted to the EMBL Data Library, August 1997
 A; Reference number: Z20343
 A; Accession: T27319
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-656 <WIL>
 A; Cross-references: EMBL:298877; PIDN:CA54473.1; GSFDB:GN00023; CESP:Y69H2.3b
 A; Experimental source: clone Y69H2
 C; Genetics:
 A; Gene: CESP:Y69H2.3b
 A; Map position: 5
 A; Introns: 183/1; 247/1; 312/1; 353/1; 383/1; 429/1; 453/2; 522/1; 586/3
 Query Match Score 30.2%; DB 2; Length 626;
 Best Local Similarity 36.8%; Pred. No. 0.00026;
 Matches 21; Conservative 11; Mismatches 23; Indels 2; Gaps 2;

Qy 12 CPSNEIFSRCDGRC-QRFCPNVPKPLCIKICAPGCVCRUGYLRNKKVYPRSKC 66
 Db 123 CPVNEVSNECHNPCTEKCPKNAPOVNCLMACQVGSCMDGFVRNNQGVCKEAC 179

RESULT 4
 alpha tectorin - mouse
 C; Species: *Mus musculus* (house mouse)
 C; Date: 22-Oct-1999 # sequence_revision 22-Oct-1999 # text_change 21-Jul-2000
 R; Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.
 J. Biol. Chem. 271, 891-8801, 1997
 A; Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to connexins
 A; Reference number: Z20771; MUID:97236841; PMID:9079715
 A; Accession: T30197
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-2155 <LEG>
 A; Cross-references: EMBL:X99805; PID:91915908; PIDN:CAA68138.1; PID:91915909
 A; Experimental source: strain CD1; whole cochlea
 A; Note: non-collagenous protein only expressed in the inner ear, by cells both in and surrounding the inner ear
 Query Match Score 28.9%; DB 2; Length 2155;
 Best Local Similarity 38.6%; Pred. No. 0.002;
 Matches 22; Conservative 7; Mismatches 26; Indels 2; Gaps 2;

Qy 11 KCP5NEIFSRCDGRC-QRFCPNVPKPLCIKICAPGCVCRUGYLRNKKVYPRSKC 67
 Db 983 ECPEASHFEEC-MTCETCTALGPICVDSCSEGQQCDEGY-RUQGSQCVRSECG 1037

RESULT 5
 T42215
 zonadhesin - mouse
 N; Alternative names: sperm-specific membrane protein
 C; Species: *Mus musculus* (house mouse)
 C; Date: 03-Dec-1999 # sequence_revision 03-Dec-1999 # text_change 03-Dec-1999

C; Accession: T42215
 R; Gao, Z.; Garbers, D.L.
 J. Biol. Chem. 273, 3415-3421, 1998
 A; Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein
 A; Reference number: Z22080; MUID:9812314; PMID:952463
 A; Accession: T42215
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-5376 <GAO>
 A; Cross-references: EMBL:U97068; PID:93327421; PIDN: AAC26680.1
 A; Genetics:
 A; Gene: Zan
 A; Map position: 5
 A; Function: functions in multiple cell adhesion processes
 A; Description: found exclusively on the apical region of the sperm head
 A; Note: found exclusively on the apical region of the sperm head
 C; Keywords: cell adhesion

Query Match Score 28.9%; DB 2; Length 5376;
 Best Local Similarity 37.5%; Pred. No. 0.004;
 Matches 24; Conservative 8; Mismatches 22; Indels 10; Gaps 3;

Qy 11 KCP5NEIFSRCDGRC-QRFCPNVPKPLC-----IKICAPGCVCRUGYLRNKKVYPRSKC 63
 Db 4743 KCPA5NSLYTHCLPCLPSCSN - PDGRCEGTSHKAPSTCRGCVCPGYLLN-KDTCVHK 4799
 Qy 64 SKCG 67
 Db 4800 NCAG 4803

RESULT 6
 H89044
 Query Match Score 118; DB 12 [Imported] - *Caenorhabditis elegans*
 Protein B0738.12 [Imported] - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 10-May-2001 # sequence_revision 10-May-2001 # text_change 10-May-2001
 C; Accession: H89044
 R; anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A; Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A; Reference number: A75000; MUID:99069613; PMID:9851916
 A; Note: see websites genome.wustl.edu/gsc/C-elegans and www_sanger.ac.uk/projects/C-elegans
 A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
 A; Accession: H89044
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-166 <STO>
 A; Cross-references: GB:chr_V; PID:92315490; GSPDB:GN00023; CESP:B023
 C; Genetics:
 A; Gene: B0238.12
 A; Map position: 5

Query Match Score 28.8%; DB 2; Length 166;
 Best Local Similarity 36.8%; Pred. No. 0.00042;
 Matches 25; Conservative 11; Mismatches 25; Indels 7; Gaps 4;

Qy 4 GGLGGRKCP---SNETFSRCDGRCORFCPNVPKPLCIKICAPG-CYVRLGFLRNK-KK 58
 Db 27 GQYGGGRLPGRNRBEYKTGTACEPSCTN - PNPMCFKQC1INNVQCRSGYVRNEITP 84
 Qy 59 VCUPRSKC 66
 Db 85 QCVRQAQC 92

RESULT 7
 T24293
 hypothetical protein T01D3.3a - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 # sequence_revision 15-Oct-1999 # text_change 15-Oct-1999

R; Stewart, C.
 Submitted to the EMBL Data Library, October 1996

A; Reference number: 219870
A; Accession: T24293
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-802 <WIL>
A; Cross references: EMBL:Z81110; PIDN:CA03259..1; GSPDB:GN00023; CESP:T01D3..3a
A; Experimental source: clone T01D3
A; Genetics:
A; Gene: CESP:T01D3..3a
A; Map position: 5
A; Introns: 74/1; 121/1; 200/2; 493/1; 673/3; 772/2

Query Match 28.0%; Score 109.5; DB 2; Length 802;
Best Local Similarity 39.0%; Pred. No. 0.0021;
Matches 23; Conservative 7; Mismatches 24; Indels 5; Gaps 3;

Qy 12 CPSNEIFSRCDGRQFCRCPNVPKPKLC-IKICAPGVCRGLYLR--NNKKVCPYRSKC 66
Db 82 CGANEQYSACFSSCOPSCQD-PSTPACPAPGCGCTLPGYIRRDPSSPRSACVPRGLC 139

RESULT 8

T24294 hypothetical protein T01D3..3b - Caenorhabditis elegans
A; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C; Accession: T24294
R; Steward, C.
Submitted to the EMBL Data Library, October 1996
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-949 <WIL>
A; Cross references: EMBL:Z81110; PIDN:CA03260..1; GSPDB:GN00023; CESP:T01D3..3b
A; Experimental source: clone T01D3
C; Genetics:
A; Gene: CESP:T01D3..3b
A; Map position: 5
A; Introns: 74/1; 126/1; 161/2; 221/1; 268/1; 347/2; 640/1; 820/3; 919/2

Query Match 28.0%; Score 109.5; DB 2; Length 949;
Best Local Similarity 39.0%; Pred. No. 0.0024;
Matches 23; Conservative 7; Mismatches 24; Indels 5; Gaps 3;

Qy 12 CPSNEIFSRCDGRQFCRCPNVPKPKLC-IKICAPGVCRGLYLR--NNKKVCPYRSKC 66
Db 229 CGANEQYSACFSSCOPSCQD-PSTPACPAPGCGCTLPGYIRRDPSSPRSACVPRGLC 286

RESULT 9

T34022 zonadhesin - pig
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000
C; Accession: T34022
R; Hardy, D.M.; Garbers, D.L.
A; Title: A sperm membrane protein that binds in a species-specific manner to the egg ext
A; Reference number: Z21464;
A; Accession: T34022
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Cross references: EMBL:U40024; NID:g1066465; PID:g1066466; PMID:792795
A; Experimental source: strain Meishan; testis
C; Genetics:
A; Gene: Zan
C; Function:
A; Description: may be involved in sperm adhesion to the zona pellucida

Query Match 27.5%; Score 107.5; DB 2; Length 2476;
Best Local Similarity 33.3%; Pred. No. 0.0077;

Matches 22; Conservative 9; Mismatches 18; Indels 17; Gaps 3;

Qy 11 KCPSENIEFSRCDGRQFCRCPNVPKPLCIKICAPGVCRGLYLNKKVCPV 61
Db 1455 KCPSSSYYSTCANPPATCLSLNNPSYCPSLTP-----CAESCEQKGHILLSGTS-CV 1506

Qy 62 PRSKCG 67
Db 1507 PLSQCG 1512

RESULT 10

T15609 hypothetical protein C25E10.8 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C; Accession: T15609
R; Bradshaw, H.
Submitted to the EMBL Data Library, February 1996
A; Description: The sequence of C. elegans cosmid C25E10.
A; Reference number: Z18376
A; Accession: T15609
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1..37 <BRA>
A; Cross-references: EMBL:U50311; NID:g1226295; PID:g1226303; PTDN:AAA92313..1; CESP:K2

Query Match 25.7%; Score 100.5; DB 2; Length 137;
Best Local Similarity 36.8%; Pred. No. 0.0044;
Matches 21; Conservative 7; Mismatches 26; Indels 3; Gaps 3;

Qy 11 KCPSENIEFSRCDGRQFCRCPNVPKPLCIKICAPGVCRGLYLNKKVCPVRSKC 66
Db 81 KCPENETFFRCGTACEPTCKBGPDRP-CTROCTVNVCOSSGFVRNGYR-CTBLKEC 135

RESULT 11

T16574 hypothetical protein K05F1.10 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C; Accession: T16574
R; Wohldmann, P.
Submitted to the EMBL Data Library, June 1995
A; Description: The sequence of C. elegans cosmid K05F1.
A; Reference number: Z18377
A; Accession: T16574
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1..140 <WHP>
A; Cross-references: EMBL:U29377; NID:g868173; PID:g868180; PTDN:AAA68717..1; CESP:K05F1

Query Match 25.6%; Score 100; DB 2; Length 140;
Best Local Similarity 32.8%; Pred. No. 0.005;
Matches 21; Conservative 10; Mismatches 25; Indels 8; Gaps 2;

Qy 11 KCPSENIEFSRCDGRQFCRCPNVPKPLCIKICAPGVCRGLYLNKKVCPV 62
Db 52 ECQREHHHLJCGPBRHCDTCEENIFSPPHCLNLHAXCYFPRCVNDGYVRSEKGICIR 111

Qy 63 RSKC 66
Db 112 PSHC 115

- RESULT 12**
- VRHUU von Willebrand factor precursor - human
- C:Species: Homo sapiens (man)
- C:Date: 04-Dec-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
- C:Accession: A34480; S02377; A37139; S23676; A25298; A23366; S23618; S23645; A94R; Mancuso, D.J.; Tulley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sora J.J. Biol. Chem. 264, 19514-19527, 1989
- A:Title: Structure of the gene for human von Willebrand factor.
- A:Reference number: A34480; PMID:90062044; PMID:2584182
- A:Molecule type: DNA
- A:Cross-references: EMBL: M25864
- A:Residues: 1-2813 <JAN>
- R:Bonthron, D.; Orkin, S.H.
- Eur. J. Biochem. 171, 51-57, 1988
- A:Title: The human von Willebrand factor gene. Structure of the 5' region.
- A:Reference number: S02377; PMID:8811704; PMID:2828057
- A:Molecule type: DNA
- A:Residues: 1-177 <BO2>
- A:Cross-references: EMBL: X06828
- R:Mancuso, D.J.; Tulley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sora R:Bonthron, D.; Orkin, S.H.
- Biochemistry 30, 253-269, 1991
- A:Title: Human von Willebrand factor gene and pseudogene: structural analysis and difference from the mouse gene.
- A:Reference number: A37139; PMID:91105089; PMID:1988024
- A:Accession: A37139
- A:Molecule type: DNA
- A:Residues: 990-1947 <MAD>
- A:Cross-references: CB: M60675; NID: 9340357; PIDN: AAA61295.1; PMID: 9553810
- A:Note: the authors translated the codon CGC for residue 156 as Gln
- R:Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Raveria, C.P.; Morin, M.J.; Dombalagian, Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
- A:Title: Molecular cloning of the human gene for von Willebrand factor and identification of the gene for the mouse gene.
- A:Reference number: S23676; PMID:87260814; PMID:3496594
- A:Accession: S23676
- A:Molecule type: DNA
- A:Residues: 2731-2813 <COL>
- A:Cross-references: EMBL: M16945
- R:Bonthron, D.; Orr, E.C.; Mitsoch, L.M.; Ginsburg, D.; Hardin, R.I.; Orkin, S.H.
- Nucleic Acids Res. 14, 7125-7127, 1986
- A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
- A:Reference number: A25298; PMID:3489923
- A:Accession: A23298
- A:Molecule type: mRNA
- A:Residues: 1-470, 'V', 472-2813 <BON>
- A:Cross-references: EMBL: X04355
- R:Verweij, C.L.; Diergaard, P.J.; Hart, M.; Pannekoek, H.
- EMBO J. 5, 1839-1847, 1986
- A:Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protein.
- A:Reference number: A91044; PMID:87004550; PMID:3019665
- A:Accession: A23469
- A:Molecule type: mRNA
- A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>
- A:Cross-references: EMBL: X04146
- R:Verweij, C.L.; Diergaard, P.J.; Hart, M.; Pannekoek, H.
- EMBO J. 5, 3074, 1986
- A:Reference number: A91056
- A:Accession: A23466
- A:Molecule type: mRNA
- A:Residues: 1021-1030 <VE2>
- A:Note: this is a revision to the sequence from reference A91044
- R:Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.
- Biochem. Biophys. Res. Commun. 144, 657-665, 1987
- A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated A:Reference number: S23618; PMID:3495233; PMID:3495236
- A:Accession: S22618
- A:Molecule type: mRNA
- A:Residues: 1-120 <SH2>
- A:Cross-references: EMBL: M17388; NID: 9799330; PIDN: AAA65940.1; PMID: 9340316
- A:Accession: S21645
- A:Molecule type: protein
- A:Residues: 23-56 <SH3>
- R:Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
- A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand factor.
- A:Accession number: A94060; PMID:86016708; PMID:2866688
- A:Accession: A94060
- A:Molecule type: mRNA
- A:Residues: 'WA', '739, 'C', '744-769, 'H', 771-788, 'A', 790-803, 'S', 805-873; 1289-1471, 'D', 14
- A:Note: the authors translated the codon TCG for residue 2168 as Cys
- R:Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.
- Biochemistry 25, 3164-3171, 1986
- A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated A:Reference number: A90504; PMID: 86269894; PMID: 3488076
- A:Accession: A90504
- A:Molecule type: mRNA
- A:Residues: 781-788, 'A', 790-1424 <SH>
- A:Note: 852-Gln, 857-Asp, and 1381-Thr were also found
- R:Ginsburg, D.; Hardin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.
- Science 228, 1401-1406, 1985
- A:Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clone A:Accession number: A44178; PMID: 384428
- A:Accession: A44178
- A:Molecule type: mRNA
- A:Residues: 2621-2813 <GIN>
- A:Cross-references: EMBL: K03028; NID: 9340308; PIDN: CAA26503.1; PMID: 9340309
- R:Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; Nucleic Acids Res. 13, 4699-4717, 1985
- A:Title: Construction of cDNA coding for human von Willebrand factor using antibody P
- A:Reference number: S07363; PMID: 85269603; PMID: 3875078
- A:Accession: S07363
- A:Molecule type: mRNA
- A:Residues: 2731-2813 <VE3>
- A:Cross-references: EMBL: X02672; NID: 937939; PIDN: CAA26503.1; PMID: 937940
- R:Lynch, D.C.; Zimmerman, T.S.; Wade, R.D.; Ashida, K.; Ling, E.H.; Li Cell 41, 49-56, 1985
- A:Title: Molecular cloning of cDNA for human von Willebrand factor.
- A:Reference number: S23678; PMID: 85201687; PMID: 3873280
- A:Accession: S23678
- A:Molecule type: mRNA
- A:Residues: 2731-2813 <LYN>
- A:Cross-references: EMBL: K03028
- R:Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.
- Biochemistry 25, 3171-3184, 1986
- A:Title: Amino acid sequences of human von Willebrand factor.
- A:Reference number: A90505; PMID: 3524673
- A:Accession: A90505
- A:Molecule type: Protein
- A:Residues: 764-788, 'A', 790-1471, 'D', 1473-2813 <TP>
- A:Note: 789-Thr was also found
- R:Chopet, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.
- Biochemistry 25, 3146-3155, 1986
- A:Title: Human von Willebrand factor: a multivalent protein composed of identical subunits.
- A:Reference number: A36013; PMID: 3015199
- A:Accession: A36013
- A:Molecule type: Protein
- A:Residues: 64-773; 2803-2813 <CHO>
- R:Dent, J.A.; Berlowitz, D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.
- Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
- A:Title: Identification of a cleavage site directing the immunochemical detection of A:Reference number: A36013; PMID: 90349604; PMID: 2385594
- A:Accession: A36013
- A:Molecule type: Protein
- A:Residues: 1606-1617 <DEN>
- R:Ray, P.J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Ohlsson-Wilhelm, B.
- Science 232, 995-998, 1986
- A:Title: Propolypeptide of von Willebrand factor circulates in blood and is identical A:Reference number: A60913; PMID: 86208144; PMID: 3486471
- A:Accession: A60913
- A:Molecule type: protein
- A:Residues: 576-590 <PAPY>
- C:Genetic CS:
- A:Gene: GDB: VWF
- A:Cross-references: GDB: 119125; OMIM: 193400

A; Map position: 12p13.3-12p13.2
 A; Introns: 19/1; 74/1; 108/2; 292/1; 219/3; 333/1; 370/2; 386/1; 431/3; 478/1; 51
 52/1; 1724/1; 1771/1; 1819/1; 1874/1; 1889/1; 1949/1; 2021/3; 2194/1; 2206/1; 230
 C; Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
 R; Pancer, Z.; Rast, J.P.; Davidson, E.H.
 C; Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicate
 A; Title: Origins of immunity: transcription factors and homologs of effector genes of
 F; 1-22/Domain: signal sequence #status predicted <SIG>
 F; 23-763/Product: von Willebrand antigen II #status predicted <NA1>
 F; 34-366/Domain: type D repeat 1 <DB1>
 F; 387-745/Domain: type D repeat 2 <DB2>
 F; 698-700/Region: cell attachment (R-G-D) motif
 F; 764-865/Domain: von Willebrand factor #status predicted <MA2>
 F; 784-833/Region: duplication
 F; 788-833/216-2261/Region: duplication
 F; 842-1130-1934-2203/Region: duplication on
 F; 866-1241/Domain: type D repeat 3 <DD3>
 F; 1275-1443/Domain: von Willebrand factor type A repeat homology <VWA1>
 F; 1496-1654/Domain: von Willebrand factor type A repeat homology <VWA2>
 F; 1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>
 F; 2296-2330/Domain: type D repeat 4 <DD4>
 F; 2340-2365/Domain: type B repeat 1 <VB1>
 F; 2375-2399/Domain: type B repeat 2 <VB2>
 F; 2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>
 F; 2507-2509/Region: cell attachment (R-G-D) motif
 F; 2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
 F; 857-1231-1515-1574-2223-2290-2357-2400-2546-2585-2790/Binding site: carbohydrate (Asn)
 F; 1147/Binding site: carbohydrate (Asn) (covalent) #status atypical
 F; 1248-1256-1468-1477-1487-1679-2298/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F; 1263-1486/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match Score 98; DB 1; Length 2813;
 Best Local Similarity 26.0%; Pred. No. 0.073;
 Matches 19; Conservative 13; Mismatches 27; Indels 14; Gaps 2;

Qy 8 GRG-----KCPSENEIFSRCDGRQRFCPNV-VPKPLC1K1KICAPGCYCRGLGYL 53
 Db 635 GRGVRYAWEPRGRCLENCPKQVYLQCGTPCNLTCSRSLSTPDEECALEGCFCPGGLY 694

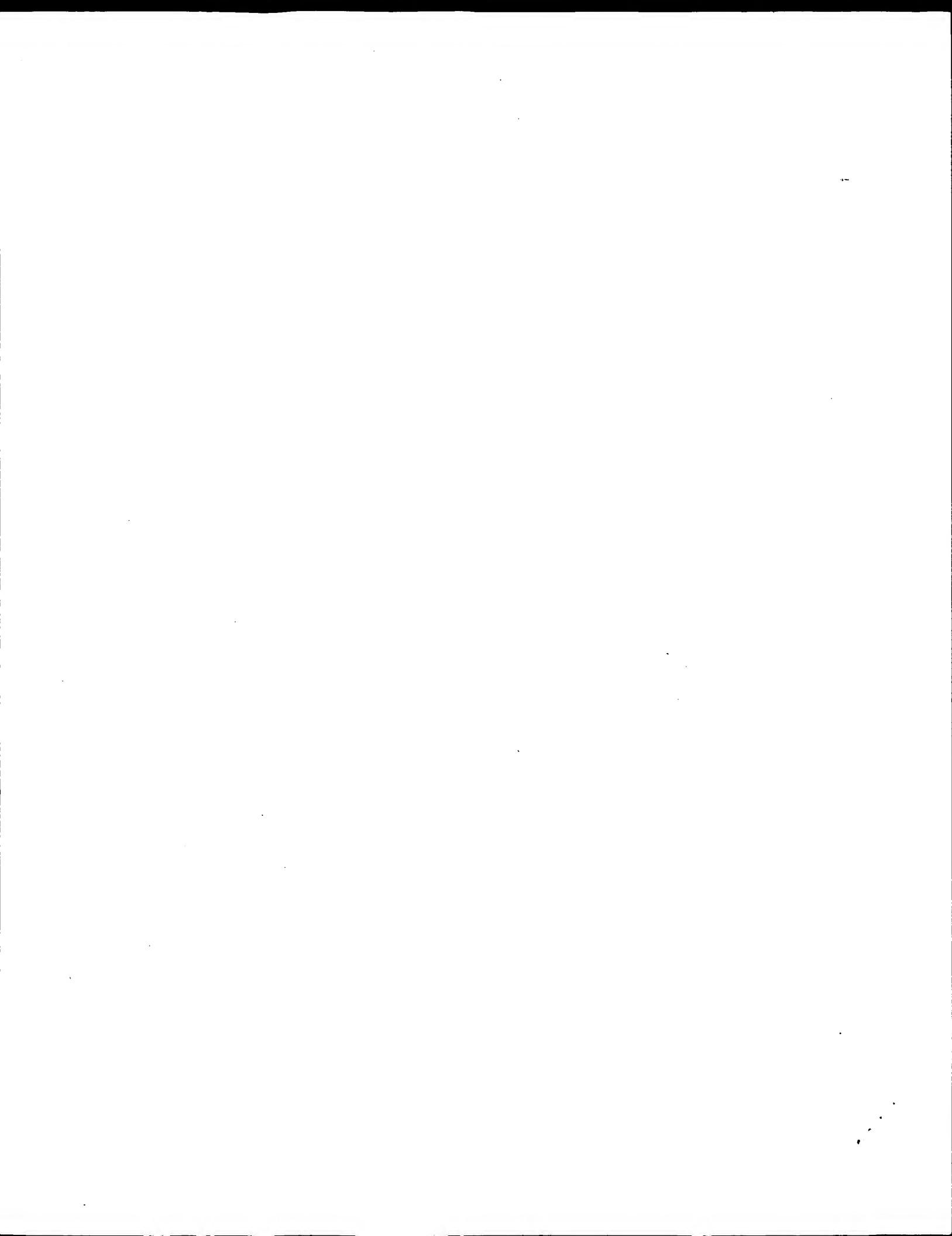
Qy 54 RNKKKVCPREKC 66
 Db 695 MDERGDCVKQAQ 707

RESULT 13
 T30243
 alpha tectorin - chicken
 C; species: Gallus gallus (chicken)
 C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
 C; Accession: T30243
 R; Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.
 Hear. Res. 130, 62-74, 1999
 A; Title: Chick alpha tectorin: molecular cloning and expression during embryogenesis.
 A; Reference number: z20783; PMID:9925181; PMID:10320099
 A; Accession: T30243
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-2120 <COU>
 A; Cross-references: EMBL:AJ012287; NID:e1361091; PID:e1361092; PIDN:CAA09979.1
 A; Note: non-collagenous protein only expressed in the inner ear

Query Match Score 97.5; DB 2; Length 2120;
 Best Local Similarity 35.7%; Pred. No. 0.066;
 Matches 20; Conservative 6; Mismatches 29; Indels 1; Gaps 1;

Qy 12 CPSNEIFSRCDGRQRFCPNVVPKPLC1K1KICAPGCYCRGLGYLNRKKVCPREKC 67
 Db 1345 CPPNSHYECSVLSLCOPRCAAIRLSDCGHYCVEGOCDPGYVLNGSKCLPQN-G 1399

RESULT 14
 T17405
 scavenger receptor cysteine-rich protein - sea urchin (Strongylocentrotus purp



Result No.	Score	Query	Match Length	DB ID	Description
1	113	28.9	5376	1 ZAN_MOUSE	088799 mus musculus
2	109	27.9	2700	1 ZAN_HUMAN	O93493 homo sapiens
3	107.5	27.5	2476	1 ZAN_PIG	Q28983 sus scrofa
4	104.5	26.7	56	1 AMCI_APIME	P5662 apis mellifera
5	103.5	26.5	2813	1 VWF_CANFA	P28295 canis familiaris
6	101.5	26.0	937	1 VWF_BOVIN	P80012 bos taurus
7	98.5	25.2	2282	1 ZAN_RABBIT	P57599 oryctolagus cuniculus
8	98	25.1	1115	1 A62F_DROME	O46202 drosophila melanogaster
9	98	25.1	2813	1 VWF_HUMAN	P04275 homo sapiens
10	91.5	23.4	2482	1 VWF_PIG	Q28833 sus scrofa
11	90.5	23.1	3133	1 HMCT_BOMMO	P98092 bombyx mori
12	86	22.0	1700	1 BAR3_CHITE	Q03376 chironomus thummi
13	80.5	20.6	63	1 ICE1_ASCSU	P07851 ascaris suum
14	80.5	20.6	99	1 YOJ2_CAEEL	P34525 caenorhabditis elegans
15	80	20.5	1370	1 IG1R_FAT	P24062 ratmus norvegicus
16	80	20.5	1373	1 IG1R_MOUSE	Q60751 mus musculus
17	79.5	20.3	351	1 CRMB_COWPX	P73559 cowpox virus
18	78.5	20.1	65	1 ICE2_ASCSU	P07852 ascaris suum
19	76.5	19.6	72	1 MT1A_MYTED	P80246 mytilus edulis
20	76.5	19.6	349	1 CRMB_CAMP	Q62554 mytilus edulis
21	76.5	19.6	855	1 ST14_MOUSE	P56677 mus musculus
22	75.5	19.6	349	1 CRMB_YARV	P34015 variola virus
23	75.5	19.3	5179	1 MUC2_HUMAN	Q02817 homo sapiens
24	75.5	19.3	956	1 TSP3_MOUSE	Q95895 mus musculus
25	75	19.2	4289	1 TENX_HUMAN	P22105 homo sapiens
26	75	19.2	72	1 MT1B_MYTED	P52725 perca fluviatilis
27	73	18.7	60	1 MTL_PFLAE	Q63610 caenorhabditis elegans
28	72.5	18.5	1416	1 YN81_CAEEL	P29825 myxoma virus
29	72	18.4	326	1 VT2_MXV	P43746 homo sapiens
30	72	18.4	956	1 TSP3_HUMAN	P08069 homo sapiens
31	72	18.4	1367	1 IG1R_HUMAN	Q29116 sus scrofa
32	71	18.2	1746	1 TENA_PIG	P19398 ascaris suum
33	70.5	18.2	62	1 ITR1_ASCSU	

GenCore version 5.1.3
Copyright (C) 1993 - 2003 Compugen Ltd.
OM protein - protein search, using sw model
Run on: February 26, 2003, 15:03:22 ; Search time 29 Seconds
(without alignments)
95.825 Million cell updates/sec

Title: US-09-506-978-1
Perfect score: 391
Sequence: 1 GGFGLGGRKCPNSNETFSR.....CRLGYLRNKKKKVPRSKCG 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3

RESULT 1
ZAN_MOUSE
ID ZAN_MOUSE STANDARD; PRT; 5376 AA.
AC 088799; 008647; PRT; 5376 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Zonadhesin precursor.

ZAN,
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE-98123114; PubMed=9452463;
RA Gao Z., Garbers D.L.;
RT "Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like domains";
RT domains;
RT J. Biol. Chem. 273:3415-3421(1998).
RL J. Biol. Chem. 273:3415-3421(1998).
RN [2]
RP SEQUENCE OF 4864-5376 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE-9271566; PubMed=9126492;
RA Gao Z., Harumi T., Garbers D.L.;
RT "Chromosome localization of the mouse zonadhesin gene (ZAN)." ;
RT zonadhesin gene (ZAN)." ;
RL Genomics 41:119-122(1997).
CC -!
RT FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR SIGNALING.
CC -!
SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
CC -!
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD.
CC -!
TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
CC -!
DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE ZONA PELLUCIDA.
CC -!
DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
CC -!
DOMAIN: THE WVF DOMAIN IN THE OVIDUCTAL ISTHMUS.
CC -!
OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
CC -!
SIMILARITY: CONTAINS 3 MAM DOMAINS.
CC -!
SIMILARITY: CONTAINS 25 WVF DOMAINS.
CC -!
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

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CC	^ APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).	QY	60 CVPRSKCG 67
CC	-! TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.	Db	1111:11 2224 CVPRSKCG 2231
CC	-! DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.		
CC	-! DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESTION TO THE OVIDUCTAL ISTMUS.		
CC	-! DOMAIN: THE WVF DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).		
CC	-! DOMAIN: CONTAINS 3.5 MAM DOMAINS.		
CC	-! SIMILARITY: CONTAINS 4.5 WVF DOMAINS.		
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CC	DR AF033356; AAC51208.1; -.		
DR	DR 083191; AAC51208.1; -.		
DR	DR Geneva; HGNC:12857; ZAN.		
DR	DR MM: 602372; -.		
DR	DR InterPro: IPRO00561; EGF-like.		
DR	DR InterPro: IPRO00998; MAM domain.		
DR	DR InterPro: IPRO02919; TIL_Cysrich.		
DR	DR InterPro: IPRO03328; TIL_Cysrich.		
DR	DR InterPro: PF00094; wvd; 4.		
DR	DR InterPro: PF00629; MAM; 4.		
DR	DR Pfam: PF01826; TIL; 5.		
DR	DR Pfam: PF02345; TIL; 4.		
DR	SMART: SM00216; WVD; 1.		
DR	DR PROSITE: PS01186; EGF_2; 3.		
DR	DR PROSITE: PS00740; MAM_1; 1.		
DR	DR PROSITE: PS50050; MAM_2; 4.		
KW	KW Glycoprotein; Transmembrane; Cell adhesion; Repeat.		
FT	FT NON-TER		
FT	FT DOMAIN <1 109 MAM 1.		
FT	FT DOMAIN 112 136 MAM 2 (PARTIAL).		
FT	FT DOMAIN 161 326 MAM 3.		
FT	FT DOMAIN 322 446 MAM 4.		
FT	FT DOMAIN 483 951 66 X HEPTAPEPTIDE REPEATS (APPROXIMATE) (MUCIN-LIKE DOMAIN).		
FT	FT DOMAIN 953 1065 WVF 1 (PARTIAL).		
FT	FT DOMAIN 1066 1454 WVF 2.		
FT	FT DOMAIN 1455 1861 WVF 3.		
FT	FT DOMAIN 1862 2292 WVF 4.		
FT	FT DOMAIN 2293 2684 WVF 5.		
FT	FT DOMAIN ? ? EGF-LIKE.		
FT	FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 403 403 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 1023 1023 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 1099 1099 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 1618 1618 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 1737 1737 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 1832 1832 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 1878 1878 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 2136 2136 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CARBOHYD 2505 2505 N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	FT CONFLICT 2374 2379 NNQKMA -> RAGFGP (IN REF. 1).		
SQ	SQ SEQUENCE 2700 AA; 293013 MW; 80E60CC0B12277B1 CRC64;		
Query Match	27 98; Score 109; DB 1; Length 2700;		
Best Local Similarity	35 38; Pred. No. 0.0052;		
Matches 24;	Conservative 11; Mismatches 13; Indels 20; Gaps 4;		
Qy	11 KCPSEIFPRC-----DGRQRCPNVPKPLICAPGEVRLRNKKV 59		
Db	2173 ECPAYSSYTNCPLSCSPSSWDLGRCE--GAKVP---SACAEKGTCQPGYVLSEDK- 2223		

FT	DOMAIN	841	>937	VWFED 3.	
FT	STATE	410	410	FACTOR XIIIa-BINDING.	
FT	STATE	414	414	FACTOR XIIIa-BINDING.	
FT	STATE	605	605	FACTOR XIIIa-BINDING.	
FT	DISULFID	766	807	BY SIMILARITY	
FT	DISULFID	775	803	BY SIMILARITY	
FT	DISULFID	913	920	BY SIMILARITY	
FT	CARBOPHYD	99	99	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOPHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOPHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOPHYD	665	665	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOPHYD	856	856	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CONFLICT	330	330	MISSING (IN REF. 3).	
FT	CONFLICT	523	523	MISSING (IN REF. 4).	
FT	CONFLICT	528	528	G -> Q (IN REF. 4).	
FT	NON-TER	937	937		
SQ	SEQUENCE	937 AA:	102599 MW:	9BF4C94A25A5629 CRC64;	
Query	Match	26	0%	Score 101.5 : DB 1; Length 937;	
Best Local Similarity		28.68		Pred. No. 0.0014;	
Matches	16:	Conservative	13:	Mismatches 26: Indels 1; Gaps 1	
Qy	12	CPSNBIFSRCDGRQRFCRPNV - PKPLKIKICAPGCVCRGLYLRNKKVCPRSK 66			
Db	651	CPHG4YQQCGTPCENLTCRLSHPDEECTEVCLEGCFPPQLFLDERTSCVPKAQ 706			
RESULT 7					
ZAN_RABIT		STANDARD;	PRT:	2282 AA.	
ID	ZAN_RABIT				
AC	P57939;				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	15-JUN-2002	(Rel. 41, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Zonadhesin (Fragment).				
GN	ZAN.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.				
NCBI-TaxID	9986;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TESTS=Tests;				
RX	PTSSURF=21573741; PubMed=11717130;				
RA	Le I.A., Sivashannugam P., O'Rand M.G.;				
RA	"zonadhesin": characterization, localization, and zona pellucida binding."				
RT					
RL	Biol. Reprod. 65:1691-1700(2001)				
CC	-1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR SIGNALING (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: PROBABLY FORMS COVALENT OLIGOMERS (BY SIMILARITY).				
CC	-1- "zonadhesin": characterization, localization, and zona pellucida binding."				
CC	-1- DOMAIN: THE MAIN DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.				
CC	-1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL Isthmus.				
CC	-1- DOMAIN: THE WNF DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY) TO HUMAN INTESTINAL MUCIN MUC2).				
CC	-1- SIMILARITY: CONTAINS AT LEAST 2 MAM DOMAINS.				
CC	-1- SIMILARITY: CONTAINS 4-5 WNF DOMAINS.				
CC	-1- SIMILARITY: CONTAINS 1 EGFR-LIKE DOMAIN.				
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- CC "Evolution of human von Willebrand factor; cDNA sequence polymorphisms, repeated domains, and relationship to von Willebrand antigen II.";
 CC RT
 CC RT
 CC RL
 CC Biochem. Biophys. Res. Commun. 144: 657-665(1987).
 CC RN [4]
 CC SQUENCE OF 1-1400 FROM N.A.
 CC MEDLINE=87004550; PubMed=1019665;
 CC RX
 CC RA
 CC Verweij C.L., Diergaard P.J., Hart M., Pannenkoek H.;
 CC RT
 CC "Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protein considerably larger than the mature vWF subunit.";
 CC RN [5]
 CC EMBO J. 5:1839-1847(1986).
 CC RP
 CC ERATUM.
 CC RA
 CC Verweij C.L., Diergaard P.J., Hart M., Pannenkoek H.;
 CC RL
 CC EMBO J. 5:3074-3074(1986).
 CC RN [6]
 CC RP
 CC SEQUENCE OF 764-2813.
 CC RX
 CC MEDLINE=86269895; PubMed=3524673;
 CC RL
 CC Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,
 CC RA
 CC Walsh K.A., Chopek M.W., Sadler J.E., Fujikawa K.;
 CC RA
 CC "Amino acid sequence of human von Willebrand factor.";
 CC RT
 CC Biochemistry 25:3171-3184(1986).
 CC RL
 CC Biochemistry 25:3164-3171(1986).
 CC RN [7]
 CC RP
 CC SEQUENCE OF 781-1424 FROM N.A.
 CC RX
 CC MEDLINE=86259894; PubMed=4488076;
 CC RL
 CC Sheldon-Inloes B.B., Titani K., Sadler J.E.;
 CC RA
 CC "cDNA sequences for human von Willebrand factor reveal five types of repeated domains and five possible protein sequence polymorphisms.";
 CC RT
 CC Biochemistry 25:3164-3171(1986).
 CC RL
 CC RN [8]
 CC RP
 CC SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.
 CC RX
 CC MEDLINE=86016708; PubMed=3864688;
 CC RL
 CC Sadler J.E., Shelton-Inloes B.B., Sorace J.M., Harlan J.M.,
 CC RA
 CC Titani K., Davie E.W.;
 CC RT
 CC "Cloning and characterization of two cDNAs coding for human von Willebrand factor.";
 CC RT
 CC Proc. Natl. Acad. Sci. U.S.A. 82:6394-6398(1985).
 CC RN [9]
 CC RP
 CC SEQUENCE OF 990-1947 FROM N.A.
 CC RX
 CC MEDLINE=91105089; PubMed=1988024;
 CC RA
 CC Mancuso D.J., Tuley B.A., Westfield L.A., Lester-Mancuso T.L.,
 CC RA
 CC Le Beau M.M., Sorace J.M., Sadler J.E.;
 CC RT
 CC "Human von Willebrand factor gene and pseudogene: structural analysis and differentiation by polymerase chain reaction.";
 CC RL
 CC Biochemistry 30:253-269(1991).
 CC RN [10]
 CC RP
 CC SEQUENCE OF 2731-2813 FROM N.A.
 CC RX
 CC MEDLINE=85269603; PubMed=3875078;
 CC RA
 CC Verweij C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,
 CC RA
 CC Geurts van Kessel A., van Mourik J.A., Pannenkoek H.;
 CC RT
 CC "Construction of cDNA coding for human von Willebrand factor using antibody probes for colony-screening and mapping of the chromosomal gene.";
 CC RT
 CC Nucleic Acids Res. 13:4699-4717(1985).
 CC RN [11]
 CC RP
 CC SEQUENCE OF 1-177 FROM N.A.
 CC RX
 CC MEDLINE=88111704; PubMed=2828057;
 CC RA
 CC Bonthron D., Orkin S.H.;
 CC RT
 CC "The human von Willebrand factor gene. Structure of the 5' region.";
 CC RT
 CC Eur. J. Biochem. 171:51-57(1988).
 CC RN [12]
 CC RP
 CC SEQUENCE OF 2621-2813 FROM N.A.
 CC RX
 CC MEDLINE=85245588; PubMed=3874428;
 CC RA
 CC Ginsburg D., Handin R.I., Bonthron D.T., Donlon T.A., Bruns G.A.P.,
 CC RA
 CC Latt S.A., Orkin S.H.;
 CC RT
 CC "Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones and chromosomal localization.";
 CC RL
 CC Science 228:1401-1406(1985).
 CC RN [13]
 CC RP
 CC SEQUENCE OF 2731-2813 FROM N.A.
 CC RX
 CC MEDLINE=85201687; PubMed=3873280;
 CC RA
 CC Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,
 CC RA
 CC Ling E.H., Livingston D.M.;

- "Molecular cloning of cDNA for human von Willebrand factor authentication by a new method.";
Cell 41:49-56(1985).
RN [14]
- RP REVISIONS.
RA Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
RN [15]
- RP SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE=87260814; PubMed=3496594;
RA Collins C.J., Underdahl J.P., Levene R.B., Ravera C.P.,
Morin M.J., Dombalagian M.J., Ricca G., Livingston D.M.,
Lynch D.C.;
RA "Molecular cloning of the human gene for von Willebrand factor and identification of the transcription initiation site";
RT Proc. Natl. Acad. Sci. U.S.A. 84:4393-4397(1987).
RL [16]
- RP DISULFIDE BONDS.
RX MEDLINE=88163655; PubMed=3502076;
RA Marti T., Rosselot S.J., Titani K., Walsh K.A.;
RT "Identification of disulfide-bridged substructures within human von Willebrand factor";
RT Biochemistry 26:8090-8109(1987).
RL [17]
- RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=8274702; PubMed=3089784;
RA Samor B., Michalski J.C., Debray H., Mazurier C., Goudemand M.,
van Halbeek H., Villegenthart J.F.G., Montreuil J.;
RT "Primary structure of a new tetrantennary glycan of the N-acetylglucosaminic type isolated from human factor VIII/von Willebrand factor";
RT Eur. J. Biochem. 158:295-298(1986).
RL [18]
- RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1261-1468.
RX MEDLINE=98221174; PubMed=9553097;
RA Emsley J., Cruz M., Hanion R., Liddington R.;
RT "Crystal structure of the von Willebrand factor A1 domain and implications for the binding of platelet glycoprotein Ib.";
RT J. Biol. Chem. 273:10396-10401(1998).
RN [19]
- RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1685-1873.
RX MEDLINE=97472999; PubMed=9331419;
RA Huizinga E.G., Martijn van der Plas R., Kroon J., Sixma J.J., Gros P.;
RT "Crystal structure of the A3 domain of human von Willebrand factor: implications for collagen binding";
RT Structure 5:1147-1156(1997).
RL [20]
- RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1686-1872.
RX MEDLINE=97460108; PubMed=9312128;
RA Bienkowski J., Cruz M., Atieno A., Handin R., Liddington R.;
RT "The von Willebrand factor A3 domain does not contain a metal ion-dependent adhesion site motif";
RT J. Biol. Chem. 272:25162-25167(1997).
RN [21]
- RP VARIANT TRP-1597 AND ASP-1607.
RX MEDLINE=89264495; PubMed=2788201;
RA Ginsburg D., Ronkle B.A., Gill J.C., Montgomery R.R.,
RA Bockenstedt P.L., Johnson T.A., Yang A.Y.;
RT "Molecular basis of human von Willebrand disease: analysis of platelet von Willebrand factor mRNA";
RT Proc. Natl. Acad. Sci. U.S.A. 86:3723-3727(1989).
RN [22]
- RP VARIANT THR-1658.
RX MEDLINE=91196734; PubMed=1673047;
RA Tamuzzi M.C., Hidaka H., Boehnke M., Bruck M.E., Hanna W.T.,
RA Collins F.S., Ginsburg D.;
RT "Analysis of the relationship of von Willebrand disease (vWD) and hereditary hemorrhagic telangiectasia and identification of a potential type IIA vWD mutation (Ile865 to Thr).";
RT RL Am. J. Hum. Genet. 48:757-763(1991).
RN [23]
- RP VARIANT NORMANDY-2 AND NORMANDY-3.
RX MEDLINE=92001464; PubMed=1832934;
- RA Gaucher C., Mercier B., Jorieux S., Oufkir D., Mazurier C.;
RT "Identification of two point mutations in the von Willebrand factor gene of three families with the 'Normandy' variant of von Willebrand disease.";
RT
RL Br. J. Haematol. 78:506-514(1991).
RN [24]
- RP VARIANT CYS-1308.
RX MEDLINE=92104315; PubMed=1761120;
RA Donner M., Andersson A.-M., Kristoffersson A.-C., Nilsson L.M., Dahlback B., Holmberg L.;
RT "An Arg945->Cys515 substitution mutation of the von Willebrand factor in type IIb von Willebrand's disease.";
RT RL Eur. J. Haematol. 47:442-445(1991).
RN [25]
- RP VARIANT TRP-1306: CYS-1308 AND PRO-1613.
RX MEDLINE=91185601; PubMed=2010538;
RA Randi A.M., Rabinowitz I., Manuccio P.M., Sadler J.E.;
RT "Molecular basis of von Willebrand disease type IIb. Candidate mutations cluster in one disulfide loop between proposed platelet glycoprotein Ib binding sequences.";
RT RL J. Clin. Invest. 87:1220-1226(1991).
RN [26]
- RP VARIANT TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HIS-1399.
RX MEDLINE=91185602; PubMed=1672694;
RX MEDLINE=91185602; PubMed=1672694;
- Query Match Score 98; DB 1; Length 2813;
Best Local Similarity 26.0%; Pred. No. 0.0079;
Matches 19; Conservative 13; Mismatches 27; Indels 14; Gaps 2;
- Qy 8 GRG-----KCPSENIFSFSDGRCORFCPNV-VPKPLCLIKICAPGCYCRGLYL 53
Db 635 GRGVRVAVREPGRCELNCPKGIVLOCGTPCNLTCSRSLSPDEECNEACLEGFCFPGLY 694
- RESULT 10
- VWF_PIG STANDARD;
ID VWF_PIG
AC Q28833;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
- DE Von Willebrand factor precursor (vWF) (Fragment).
GN FBWF OR WF
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
- SEQUENCE FROM N.A.
RP Seaman W.T., Read M.S., Bellinger D.A., Nichols T.C.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
- RP SEQUENCE OF 397-553 FROM N.A.
RX MEDLINE=93356762; PubMed=352759;
RA Lavergne J.M., Piao Y.C., Ferreira V., Kerbirou-Nabias Q.,
RA Bainak B.R., Meyer D.;
RT "Primary structure of the factor VIII binding domain of human, porcine and rabbit von Willebrand factor.";
RT RL Biochem. Biophys. Res. Commun. 194:1019-1024(1993).
CC -!- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMESTASIS, IT PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF VASCULAR INJURY (BY SIMILARITY).
CC -!- SUBUNIT: MULTIMERIC (BY SIMILARITY).
CC -!- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 3 WF domains.
CC -!- SIMILARITY: CONTAINS 3 WF domains.
CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.

-!- SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.

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CC

DR EMBL; AF052036; AAC06229; 1; .

DR EMBL; S64541; AAB27829; 2; .

DR HSSP; P04275; LATZ.

DR InterPro; IPR000359; Cys_knot.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001928; Endothln_tox.

DR InterPro; IPR00064; Potato_inhibit.

DR InterPro; IPR002919; TIL_Cysrich.

DR InterPro; IPR002035; WVE_A.

DR InterPro; IPR001007; WVE_C.

DR InterPro; IPR001846; WVF_D.

DR Pfam; PF00007; CYS_knot; 1.

DR Pfam; PF00092; wva; 3.

DR Pfam; PF00093; wvc; 3.

DR Pfam; PF00094; wvd; 3.

DR Pfam; PF01826; TIL; 3.

DR PRINTS; PRO0365; ENDOTHELIN.

DR PRINTS; PRO0293; POTATOINHBT.

DR PRINTS; PRO0453; VNFA DOMAIN.

DR SMART; SM00041; CT; 1.

DR SMART; SM00181; EGF; 1.

DR SMART; SM00327; VWA; 3.

DR SMART; SM00214; VWC; 5.

DR SMART; SM00216; VWD; 3.

DR PROSITE; PS50234; VNFA; 3.

DR PROSITE; PS01208; VWF; 3.

DR PROSITE; PS01185; CTCK; 1.

DR PROSITE; PS01225; CTCK; 2.

Blood coagulation; Platelet; Glycoprotein; Extracellular matrix;

KW Plasma; Hemostasis; Repeat; cell adhesion.

FT PROTEP < 1 BY SIMILARITY.

FT CHAIN 438 437 VON WILLEBRAND FACTOR.

FT DOMAIN 62 2482 VWF D.

FT DOMAIN 438 215 AMINO-TTERMINAL.

FT DOMAIN 462 461 E1.

FT DOMAIN 500 527 CX.

FT DOMAIN 541 687 VWFED 3.

FT DOMAIN 947 1127 VWFA 1.

FT DOMAIN 1167 1334 VWF A.

FT DOMAIN 1360 1540 VWF A.

FT DOMAIN 1619 1771 VWF D.

FT DOMAIN 1885 1930 E2.

FT DOMAIN 2094 2164 VWFC 1.

FT DOMAIN 2249 2319 VWFC 2.

FT DOMAIN 2393 2481 VWFC 3.

FT SITE 2176 2178 CELL ATTACHMENT SITE (POTENTIAL).

FT DISULFID 441 482 BY SIMILARITY.

FT DISULFID 450 478 BY SIMILARITY.

FT DISULFID 484 495 BY SIMILARITY.

FT DISULFID 541 670 BY SIMILARITY.

FT DISULFID 563 705 BY SIMILARITY.

FT DISULFID 572 667 BY SIMILARITY.

FT DISULFID 588 595 BY SIMILARITY.

FT DISULFID 734 758 BY SIMILARITY.

FT DISULFID 745 785 BY SIMILARITY.

FT DISULFID 763 765 BY SIMILARITY.

FT DISULFID 827 839 BY SIMILARITY.

FT DISULFID 823 843 BY SIMILARITY.

FT DISULFID 800 804 BY SIMILARITY.

FT DISULFID 870 873 BY SIMILARITY.

FT DISULFID 908 911 BY SIMILARITY.

FT DISULFID 942 1128 BY SIMILARITY.

FT DISULFID 1338 1339 BY SIMILARITY.

FT DISULFID 1355 1541 BY SIMILARITY.

FT DISULFID 1548 1573 BY SIMILARITY.

FT DISULFID 1568 1609 OR 1611 (BY SIMILARITY).

FT DISULFID 1641 1792 BY SIMILARITY.

FT DISULFID 1619 1754 BY SIMILARITY.

FT DISULFID 1596 1757 BY SIMILARITY.

FT DISULFID 1662 1670 BY SIMILARITY.

FT DISULFID 2393 2443 BY SIMILARITY.

FT DISULFID 2408 2457 BY SIMILARITY.

FT DISULFID 2419 2473 BY SIMILARITY.

FT DISULFID 2423 2475 BY SIMILARITY.

FT DISULFID ? 2480 BY SIMILARITY.

FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 905 905 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1184 1184 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1640 1640 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1892 1892 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1959 1959 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2026 2026 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2069 2069 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2215 2215 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2254 2254 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2459 2459 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 2482 AA: 272394 MW: D4 99B7DDFB3AEDD CRC64;

Query Match Similarity 23.4%; Score 91.5; DB 1; Length 2482;

Best Local Matches 19; Conservative 11; Mismatches 31; Indels 5; Gaps 2;

Qy 2 GFGGIGGRGKPSNEIFSRCDGRQRCPNV-VPKPLKIKACAGCVCVRLGYLRNKKWC 60

Db 320 GFCAL---SCPPGQVYLLQQCTPCNLTCSRSLSYDPBECAEDCLEGCFCPPGLYLDGSGC 375

Qy 61 VPRSKC 66

Db 376 VPKAQC 381

RESULT 1.1

HMCT_BOMMO STANDARD; PRT; 3133 AA.

ID HMCT_BOMMO AC P98092; DT 01-FEB-1996 (Rel. 33, Created)

Matches 19; Last sequence update) DE Hemocytin precursor (Humoral lectin).

OS Bombyx mori (Silk moth). OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Bombyidae; Bombyx. OC Diptaria; Bombycoidea; Bombycidae; Bombyx.

NCBI_TaxID:7091; RN [1]

RP SEQUENCE FROM N.A.

RN MEDLINE=95178564; PubMed=787598;

RN [2] RA Kotani E., Yamakawa M.-I., Tashiro M., Mori H., Sumida M., RA Matsubara F., Taniai K., Kadono-Okuda K., Kato Y., Mori H.; RA Matsubara F., Yamakawa M.; RT "Cloning and expression of the gene of hemocytin, an insect humoral RT lectin which is homologous with the mammalian von Willebrand factor." RL Biochim. Biophys. Acta 1260:245-258(1995).

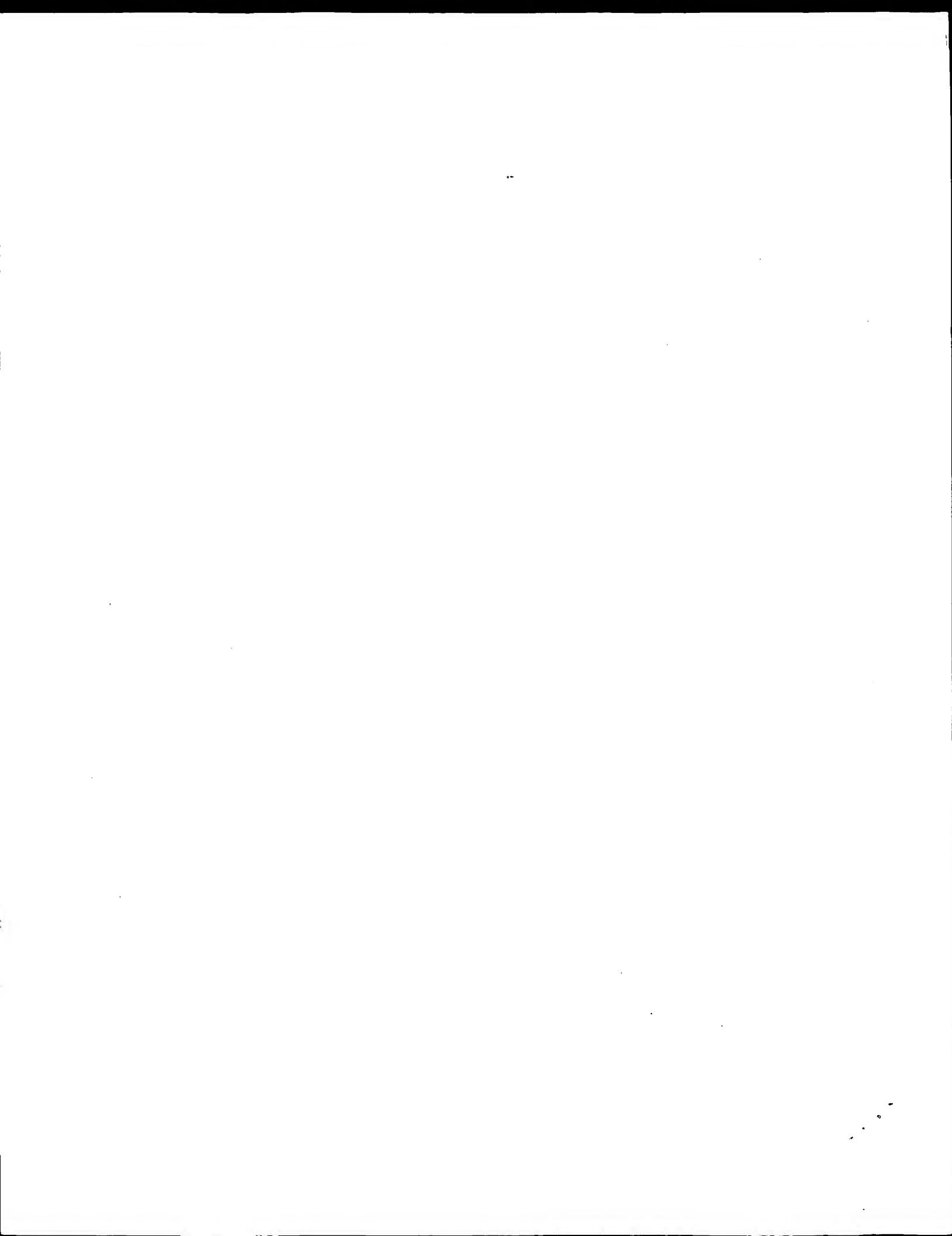
RN RA Kotani E., Iwamoto S.-I., Tashiro M., Mori H., Sumida M., RA Matsubara F., Yamakawa M.; RT Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: ADHESIVE PROTEIN AND RELATES TO HEMOSTASIS OR CC ENCAPSULATION OF FOREIGN SUBSTANCES FOR SELF-DEFENSE. CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN HEMOCYTES DURING LARVAL-PUPAL CC METAMORPHOSIS.

-!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: SALIVARY GLAND.
 CC -!- DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS.
 CC
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 DR EMBL; X52263; CNA36506_1; .
 DR PIR; S08167; S08167.
 DR HSSP; P1558; 1SKZ.
 DR InterPro; IPR004153; CXXC_repeat.
 DR Pfam; PF0128; CXXC; 71.
 KW Repeat; Signal, POTENTIAL.
 FT SIGNAL 1 20
 FT CHAIN 21 1700 BALBIAN RING PROTEIN 3.
 SQ SEQUENCE 1700 AA; 186145 MW; 34202B28521B0815 CRC64;
 Query Match 22..0%; Score 86; DB 1; Length 1700;
 Best Local Similarity 29.1%; Pred. No. 0.099; 9; Mismatches 21; Indels 6;
 Matches 23; Conservative 9; Gaps 6;
 QY 12 CPSNETFSRCDGRCFCRNVPKP-----LCIKICAPGVY---CRLGYLRNK 56
 DB 1234 CGPNQIW--CDNTRCVCPKMERPADNCKTWNDEMCQCVCKPGEPEGGCK-GVMKW 1290
 QY 57 KVCF---YPRSK----CG 67
 Db 1291 ANTSCCECPADAKPASCG 1309
 RESULT 13
 TCE1_ASCSU STANDARD; PRT; 63 AA.
 ID TCE1_ASCSU STANDARD; PRT; 63 AA.
 AC P07811;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DR Chymotrypsin/elastase inhibitor 1 (C/E-1 inhibitor).
 OS Ascaris suum (Pig roundworm) (Ascaris lumbicoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
 OC Ascarididae: Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE;
 MEDLINE=84255715; PubMed=6564898;
 RA Babin D.R., Peanassy R.J., Goos S.M.;
 RT "The iso-inhibitors of chymotrypsin/elastase from Ascaris
 lumbricoides: the primary structure.";
 RT Structure 2:679-689(1994).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
 RA MEDLINE=5006335; PubMed=792044;
 RA Huang K., Strynadka N.C., Bernard V.D., Peanassy R.J., James M.N.,
 RT "The molecular structure of the complex of Ascaris
 chymotrypsin/elastase inhibitor with porcine elastase.";
 RL Structure 2:679-689(1994).
 CC -!- FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES.
 CC -!- SIMILARITY: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.
 DR PDB: 1EAT; OS=APR-99.
 DR InterPro; IPR00219; TTL_Cysrich.
 DR Pfam; PF01826; TTL; 1.
 KW Serine protease inhibitor; 3D-structure.
 FT DISULFID 5 38
 FT DISULFID 14 33
 FT DISULFID 17 29
 FT DISULFID 21 60
 FT DISULFID 40 54

FT ACT SITE 31 32 MW; REACTIVE BOND
 SQ SEQUENCE 63 AA; 68651 MW; 5D10DE75B375F16 CRC64;
 Query Match 20..6%; Score 80.5; DB 1; Length 63;
 Best Local Similarity 30.3%; Pred. No. 0.029; 10; Mismatches 23; Indels 13; Gaps 4;
 Matches 20; Conservative 10;
 QY 8 GRGKCPNSNEIFSRCDG--RC---QRFCPNVVPKBLIKICAPGVYCRGLYLNKKYKC 60
 DB 1 GOESCGPNEVWVTECTGEMRKCGPDENTPCPLMRRPSC--ECSPG---RGMRRTNDGKC 54
 QY 61 VPRSKC 66
 DB 55 IPASQC 60
 RESULT 14
 Y002_2CAEEL STANDARD; PRT; 99 AA.
 ID Y002_2CAEEL P34625;
 AC 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 10.6 kDa protein ZK353.2 in chromosome III.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderaiae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Coppey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Hawkin P., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisteller N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Showkseen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonnhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaughan K.,
 RA Waterston R., Watson A., Wilcockson-Sproat J.,
 RA Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."
 RL Nature 368:32-38(1994).
 CC
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 CC
 DR EMBL; L15313; AAA28199_1; .
 DR WormPop; ZK353.2; CE00386.
 KW Hypothetical protein
 SQ SEQUENCE 99 AA; 10561 MW; 862659838E47E5F CRC64;
 Query Match 20..5%; Score 80.5; DB 1; Length 99;
 Best Local Similarity 28.1%; Pred. No. 0.041; 10; Mismatches 17; Indels 19; Gaps 2;
 Matches 18; Conservative 10;
 QY 1 GGFGGLGGKGPKCPSNEIFSRCDGQRFCPN-----VVPKPLCIKICA 43
 DB 31 GGYGGGGGGRGCGADNVFYR-WRCCDYSPECCIQLETWVVFLVTFIGEFFCLCACL 88
 QY 44 PGCV 47
 DB 89 AGCV 92

RESULT 15			
IG1R_RAT	STANDARD;	PRT;	1370 AA.
ID			
IG1R_RAT			
P24662;			
AC			
01-MAR-1992 (Rel. 21, Created)			
DT			
01-NOV-1997 (Rel. 35, Last sequence update)			
DT			
15-JUN-2002 (Rel. 41, Last annotation update)			
DE			
Insulin-like growth factor I receptor precursor (EC 2.7.1.112).			
GN			
IGFIR.			
Rattus norvegicus (Rat).			
Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OC			
OX			
INSB_TaxID=10116;			
RN			
SEQUENCE FROM N.A.			
RC			
TISSUE=Brain			
RX			
Medline=95277910; PubMed=7758167;			
RA			
Du J., Delafontaine P.;			
"Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA.";			
RT			
Circ. Res. 76:963-972(1995).			
RL			
[2]			
RN			
SEQUENCE OF 1-364 FROM N.A.			
RP			
STRAIN=Sprague-Dawley;			
RC			
Medline=9001496; PubMed=2477843;			
RX			
Werner H., Woloschak M., Asamo M., Shen-Orr Z., Roberts C.T. Jr.,			
RA			
Leroith D.;			
"Developmental regulation of the rat insulin-like growth factor I receptor gene.";			
RT			
Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).			
RL			
[3]			
RN			
SEQUENCE OF 913-1017 FROM N.A.			
RP			
Medline=9241245; PubMed=1530648;			
RX			
Kurachi H., Jobo K., Ota M., Kawasaki T., Itoh N.;			
RT			
"A new member of the insulin receptor family, insulin receptor-related receptor, is expressed preferentially in the kidney."			
RT			
Kidney.,"			
RL			
Biochem. Biophys. Res. Commun. 187:934-939(1992).			
CC			
-!- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I) WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.			
CC			
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC			
tyrosine phosphate.			
CC			
-!- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.			
CC			
-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC			
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN RECEPTOR SUBUNIT.			
CC			
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC			
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CC			
L22322; AAA11392; 1;			
CC			
EMBL: M27293; AAA41384; 1; -.			
DR			
PIR: A33837; A33837.			
DR			
HSSP: P02213; 1TRK.			
DR			
InterPro: IPRO00494; EGFR_L_domain.			
DR			
InterPro: IPRO0719; Euk_pk kinase.			
DR			
InterPro: IPRO02174; Furin-like.			
DR			
InterPro: IPRO02011; RPKinaseII.			
DR			
InterPro: IPRO0124; Tyr_pk kinase.			
DR			
Pfam: PF00041; fn3; 2.			
DR			
Pfam: PF00069; Pkinase_1.			
DR			
Pfam: PF00757; Furin-like; 1.			
DR			
PRINTS; PRO0109; TYRKINASE.			
DR			
ProDom: PR0000001; Euk_pk kinase.			
SMART; SMD0060; FN3; 3.			
SMART; SMD0261; TYrk; 1.			
SMART; SMD00219; Tyrc; 1.			
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.			
PROSITE; PS00239; RECEPTOR_TYR_KINASE_ITI; 1.			
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
transfase; Tyrosine-protein kinase; Receptor; Transmembrane;			
KW			
Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.			
SIGNAL	1	30	POTENTIAL-LIKE GROWTH FACTOR I RECEPTOR,
CHAIN	31	741	ALPHA-CHAIN.
FT			
FT	CHAIN	742	1370 INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
FT			BETA-CHAIN.
FT	DOMAIN	742	936 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	937	960 POTENTIAL.
FT	DOMAIN	961	1370 CITOPLASMIC (POTENTIAL).
FT	DOMAIN	608	829 FIBRONECTIN TYPE-III 1.
FT	DOMAIN	830	929 FIBRONECTIN TYPE-III 2.
FT	DOMAIN	1000	1275 PROTEIN KINASE.
FT	NP_BIND	1006	1014 ATP (BY SIMILARITY).
FT	BINDING	1034	1034 ATP (BY SIMILARITY).
FT	ACT_SITE	1136	1136 BY SIMILARITY.
FT	DISULFID	215	224 BY SIMILARITY.
FT	DISULFID	219	230 BY SIMILARITY.
FT	DISULFID	231	239 BY SIMILARITY.
FT	DISULFID	235	248 BY SIMILARITY.
FT	DISULFID	251	260 BY SIMILARITY.
FT	DISULFID	264	276 BY SIMILARITY.
FT	DISULFID	282	293 BY SIMILARITY.
FT	DISULFID	307	321 BY SIMILARITY.
FT	DISULFID	324	328 BY SIMILARITY.
FT	CARBOHYD	51	51 (POTENTIAL).
FT	CARBOHYD	102	102 (POTENTIAL).
FT	CARBOHYD	135	135 (POTENTIAL).
FT	CARBOHYD	245	245 (POTENTIAL).
FT	CARBOHYD	314	314 (POTENTIAL).
FT	CARBOHYD	418	418 (POTENTIAL).
FT	CARBOHYD	439	439 (POTENTIAL).
FT	CARBOHYD	535	535 (POTENTIAL).
FT	CARBOHYD	608	608 (POTENTIAL).
FT	CARBOHYD	623	623 (POTENTIAL).
FT	CARBOHYD	641	641 (POTENTIAL).
FT	CARBOHYD	748	748 (POTENTIAL).
FT	CARBOHYD	757	757 (POTENTIAL).
FT	CARBOHYD	765	765 (POTENTIAL).
FT	CARBOHYD	901	901 (POTENTIAL).
FT	MOD_RES	914	914 (POTENTIAL).
FT	MOD_RES	1166	1166 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CONFFLICT	985	986 AD -> PY (IN REF. 3).
FT	SEQUENCE	1370 AA;	155395 MW; A594687A41CB145 CRC64;
Query Match	20 5%	Score 80;	DB 1;
Best Local Similarity	33.8%	DB 1;	Gaps
Matches	23;	Conservative	18; Indels 22;
CC			4;
Qy	14 SNETFSRC - DGRQQRFCPNVPKPLCI --- KICAPGCV -		CGLGYL 54
Db	198 NNEYNYRCWTINRCKRMCPSCVKRACTENNECCPECLGSCHTPDDNTTCVACRHYY -		256
Qy	55 NRKKVCP 62		
Db	257 - KGVCVP 262		
Search completed: February 26, 2003, 15:04:02			
Job time : 31 secs			



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OM protein - protein search, using sw model

Run on: February 26, 2003, 15:03:23 ; Search time 29 Seconds
(without alignments)
476,040 Million cell updates/sec

Title: US-09-506-978-1

Perfect score: 391

Sequence: 1 GGEGGLGGRKCPNSNEIFSR.....CRUGYLRLNKKVCPRSKCG 67

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen Parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Databases :

- 1: SP_TREMBL_21;*
- 2: SP_archaea;*
- 3: SP_bacteria;*
- 4: SP_fungi;*
- 5: SP_invertebrate;*
- 6: SP_human;*
- 7: SP_mammal;*
- 8: SP_mhc;*
- 9: SP_organelle;*
- 10: SP_phage;*
- 11: SP_plant;*
- 12: SP_rabbit;*
- 13: SP_rat;*
- 14: SP_vertebrate;*
- 15: SP_unclassified;*
- 16: SP_virus;*
- 17: SP_archeap;*

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	133	34.0	245	5 Q19964	
2	118	30.2	561	5 Q9U1T6	caenorhabdi
3	118	30.2	626	5 Q9U1T5	caenorhabdi
4	113	28.9	2155	11 Q08523	caenorhabdi
5	113	28.9	5374	11 Q99NDO	mus musculu
6	111.5	28.5	166	5 Q16488	caenorhabdi
7	109.5	28.0	949	5 P9056	caenorhabdi
8	109	27.9	915	4 Q9BXN9	homo sapien
9	109	27.9	2601	4 Q9BZ84	homo sapien
10	109	27.9	2624	4 Q9BZ85	homo sapien
11	109	27.9	2624	4 Q96L87	homo sapien
12	109	27.9	2624	4 Q96L87	homo sapien
13	109	27.9	2689	4 Q9BZ87	homo sapien
14	109	27.9	2689	4 Q96L85	homo sapien
15	109	27.9	2721	4 Q9BZ83	homo sapien
16	109	27.9	2721	4 Q96L90	homo sapien

ALIGNMENTS

17	109	27.9	2724	4 Q9BZ88	homo sapien
18	109	27.9	2724	4 Q96L89	homo sapien
19	109	27.9	2812	4 Q9BZ86	homo sapien
20	109	27.9	2812	4 Q96L88	homo sapien
21	108	27.6	3843	5 Q9USD0	drosophila
22	108	27.6	3843	5 Q9VU94	drosophila
23	107	27.4	2155	4 Q95443	homo sapien
24	106.5	27.2	2843	4 Q9Y6R7	homo sapien
25	104.5	26.7	453	5 Q9U1U6	caenorhabdi
26	100.5	25.7	137	5 Q18157	caenorhabdi
27	100.5	25.7	211	5 Q9U1U0	caenorhabdi
28	100.5	25.7	735	4 Q95784	homo sapien
29	100	25.6	91	5 Q16938	ancylostoma
30	100	25.6	140	5 Q21248	caenorhabdi
31	99	25.3	92	5 Q9GPC4	drosophila
32	97.5	24.9	2120	13 Q9YH85	caenorhabdi
33	97	24.8	77	5 Q8T0W0	pampala hypo
34	96.5	24.7	505	5 Q25431	lytechinus
35	96.5	24.7	1036	5 Q97378	strongyloce
36	95	24.3	2108	13 Q98U19	gallus galli
37	94.5	24.2	98	5 Q94162	caenorhabdi
38	93	23.8	192	5 Q01471	caenorhabdi
39	93	23.8	1637	6 Q9XSV8	bos taurus
40	93	23.8	5146	6 Q8SPM4	bos taurus
41	92.5	23.7	108	5 Q9VUN1	drosophila
42	92.5	23.7	195	5 Q18805	caenorhabdi
43	92	23.5	249	5 Q45764	caenorhabdi
44	92	23.5	648	5 Q9NKD7	drosophila
45	92	23.5	701	5 Q9VJU4	drosophila

RESULT 1	Q19964	PRELIMINARY;	PRT;	245 AA.
ID	Q19964;			
AC	Q19964;	TREMBLE1. 01, Created)		
DT	01-NOV-1996 (TREMBLE1. 01, Last sequence update)			
DT	01-JUN-2002 (TREMBLE1. 21, Last annotation update)			
DE	F32D8.3 protein.			
GN	F32D8.3.			
OS	Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditida; Rhabditidae;			
OC	Rhabditidae; Pelerodinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Wilkinson J.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99069613; PubMed=9851916;			
RA	none;			
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology."			
RT	Science 282:2012-2018(1998).			
RL	EMBL; Z74031; CAA98455.1; .			
DR	HSSP; P56682; ICCV.			
DR	InterPro; IPR000561; EGF-like.			
DR	InterPro; IPR02919; TIL_Cysrich.			
DR	Pfam; PF01826; TLL_1.			
DR	PROSITE; PS01186; EGE_2; UNKNOWN_1.			
DR	SEQUENCE: P50186; EGE_2; UNKNOWN_1.			
SQ	SEQUENCE: 27785 MW; 781AEA77FFFE784C CRC64;			
Query Match Score 34.0%; Best Local Similarity 43.1%; Matches 28; Conservative 7; Mismatches 10; Gaps 4;				
6 LGGRGKCPNSNEIFSRDGRCQRFPPVPKPLIKCAPGVCRUGYLRNKKV-----				
57 INGEENCPMFQSFHCK-ACESTCNN--PDYCSK-CEPGCTCRNGFVRNSLKLCLVLPPE 111				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	133	34.0	245	5 Q19964	
2	118	30.2	561	5 Q9U1T6	caenorhabdi
3	118	30.2	626	5 Q9U1T5	caenorhabdi
4	113	28.9	2155	11 Q08523	caenorhabdi
5	113	28.9	5374	11 Q99NDO	mus musculu
6	111.5	28.5	166	5 Q16488	caenorhabdi
7	109.5	28.0	949	5 P9056	caenorhabdi
8	109	27.9	915	4 Q9BXN9	homo sapien
9	109	27.9	2601	4 Q9BZ84	homo sapien
10	109	27.9	2624	4 Q9BZ85	homo sapien
11	109	27.9	2624	4 Q96L87	homo sapien
12	109	27.9	2624	4 Q96L87	homo sapien
13	109	27.9	2689	4 Q9BZ87	homo sapien
14	109	27.9	2689	4 Q96L85	homo sapien
15	109	27.9	2721	4 Q9BZ83	homo sapien
16	109	27.9	2721	4 Q96L90	homo sapien

RESULT 9						
QBZB84	PRELIMINARY;	PRT;	2601	AA.		
ID Q9BZB4;						
AC Q9BZB4;						
DT 01-JUN-2001 (TRIMBLre1. 17, Created)						
DT 01-JUN-2001 (TRIMBLre1. 17, Last sequence update)						
DT 01-JUN-2002 (TRIMBLre1. 21, Last annotation update)						
DE Zonadesin variant 5.						
GN ZAN.						
OS Homo sapiens (Human).						
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.						
OX NCBI_TAXID=9606;						
RN [1]						
RP SEQUENCE FROM N.A.						
RC TISSUETESTIS;						
RA Cheung T.-L.; Wassler M.J.; Cornwall G.A.; Hardy D.M.;						
RT "Multiple Intraspecies Variants of Human Zonadhesin."						
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases						
CC -1: SIMILARITY : CONTAINS 3 DOMAIN.S						
DR AF332979; AAK01435.1; -.						
DR HSSP; P56682; ICCV						
DR InterPro; IPR00561; EGF-like.						
DR InterPro; IPR00998; MAM_domain.						
DR InterPro; IPR00965; P-rich_extrnsn.						
DR PRINTS; PRO00328; TILA_Cysrich.						
DR InterPro; IPR00919; TIL_Cysrich.						
DR InterPro; IPR001846; VWF_D.						
DR Pfam; PF00629; MAM; 3.						
DR Pfam; PF01826; TIL; 4.						
DR Pfam; PF00094; vwd; 4.						
DR PRINTS; PRO01217; PRICEXTNSN.						
DR SMART; SM00137; MAM; 3.						
DR SMART; SM00216; VWD; 4.						
DR PROSITE; PS001186; EGF_2; UNKNOWN_3.						
DR PROSITE; PS00740; MAM_1; 1.						
KW Glycoprote-in.						
SEQUENCE 2601 AA; 282429 MW; 6B97B524C67AABF4 CRC64						
Query Match 27.9%; Score 109; DB 4; Length 2601;						
Best Local Similarity 35.3%; Pred. No. 1-4e-13; Indels 20; Ga						
Matches 24; Conservative 11; Mismatches 13; Delins 1; Delins 1;						
Qy 11 KCPNSNEIFSRCS-----DGRCORFCPNVVPKPLCIKAPGCVCRIGYLRNKKV						
Db 2210 ECPDAYSYYTNCLPSCSPCDWLGRCE--GAKVP---SACAEGCICQGYVLSEDK-						
Qy 60 CVPRSKCG 67						
Db 2261 CVPRSQCG 2268						
RESULT 10						
Q96L86	PRELIMINARY;	PRT;	2601	AA.		
ID Q96L86;						
AC Q96L86;						
DT 01-DEC-2001 (TRIMBLre1. 19, Created)						
DT 01-DEC-2001 (TRIMBLre1. 19, Last sequence update)						
DT 01-JUN-2002 (TRIMBLre1. 21, Last annotation update)						
DE Zonadesin splice variant 5.						
GN ZAN.						
OS Homo sapiens (Human).						
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.						
OX NCBI_TAXID=9606;						
RN [1]						
RP SEQUENCE FROM N.A.						
RA Cheung T.-L.; Wilton M.D.; Koop B.F.; Hardy D.M.;						
RT "Genomic Basis of Inter- and Intra-species Variation in zonadesin domain structure."						

RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
-i:	SIMILARITY: CONTAINS 3 MAM_DOMAINS.
CC	EMBL: AY046055; AA04412.1; -.
DR	InterPro: IPR00561; EGF-like.
DR	InterPro: IPR00938; MAM_domain.
DR	InterPro: IPR003328; TILA_Cysrich.
DR	InterPro: IPR002919; TIL_Cysrich.
DR	InterPro: IPR001846; VWF_D.
PFam:	PF00629; MAM_3.
DR	Pfam: PF01826; TIL_4.
DR	Pfam: PF02345; TILA_4.
DR	Pfam: PF00094; vwd_4.
DR	PROSITE: PS01186; EGF_2; UNKNOWN_3.
DR	PROSITE: PS00740; MAM_1; UNKNOWN_1.
DR	PROSITE: PS50060; MAM_2; 3.
KW	Glycoprotein
SQ	SEQUENCE 2601 AA; 282353 MW; BB712962F83DE04 CRC64;
Query Match	Score 109; DB 4; Length 2601;
Best Local Similarity	27.9%; Pred. No. 1 e-05;
Matches 24;	Mismatches 11; Indels 20
Conservative	11; Mismatches 13; Indels 1
Qy	1.1 KCPNSNEIFSRK-----DGRCORFCPNVPPRPLCIRKICAPCVCRIGYLRN
Db	2210 ECPAYSSYTNCLPSCSPSCWDLDGRCE--GAKVP----SACABECICOPGYVLS
Qy	60 CVPRSKCG 67
Db	2261 CVPRSQCG 2268
RESULT 11	
Q9BZ85	PRELIMINARY; PRT; 2624 AA.
ID	QBZ85
AC	QBZ85; DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Zonadhesin variant 4.
EN	ZAN.
OC	Homo sapiens (Human)
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID	9601;
DN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-TESTIS;
RC	Cheung T.L., Wassler M.J., Cornwall G.A., Hardy D.M.; "Multiple Intra-species Variants of Human Zonadhesin." Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC	-i: SIMILARITY: CONTAINS 3 MAM_DOMAINS.
DR	EMBL: AF332978; AAC01434.1; -.
DR	INSPSP; P56622; ICCV.
DR	InterPro: IPR00561; EGF-like.
DR	InterPro: IPR000998; MAM_domain.
DR	InterPro: IPR002965; P_rich_extensn.
DR	InterPro: IPR003328; TILA_Cysrich.
DR	InterPro: IPR002919; TIL_Cysrich.
DR	InterPro: IPR001846; VWF_D.
PFam:	PF00629; MAM_3.
DR	Pfam: PF01826; TIL_4.
DR	Pfam: PF02345; TILA_4.
PFam:	PF00094; vwd_4.
DR	PRINTS: PRO1211; PRICHEXTENSIN.
DR	SMART: SM00137; MAM_3.
SMART:	SM00216; VWD_4.
DR	PROSITE: PS01186; EGF_2; UNKNOWN_3.
DR	PROSITE: PS00740; MAM_1; 1.
DR	PROSITE: PS50060; MAM_2; 3.
KW	Glycoprotein
SQ	SEQUENCE 2624 AA;
Q	27.9%; Score 109; DB 4; Length 2624;
Query Match	

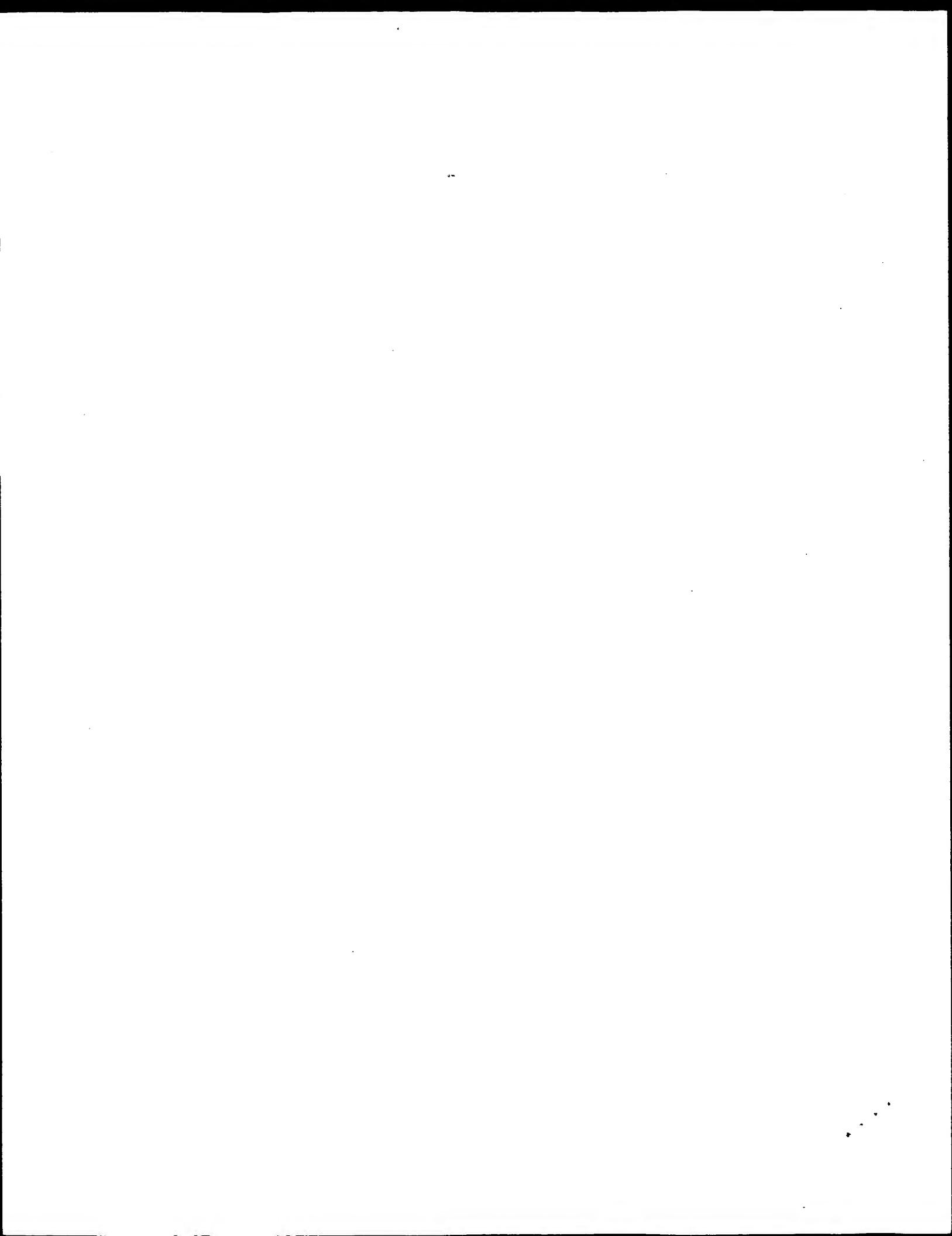
OX	NCBI_TaxID=9606;	DR	PROSITE; PS00740; MAM_1; UNKNOWN_1.
RN	[1] SEQUENCE FROM N.A.	DR	PROSITE; PS00660; MAM_2; 3.
RC	TISSUE=TESTIS;	KW	GLycoprotein;
RA	Cheung T.L., Wassler M.J., Cornwall G.A., Hardy D.M.; "Multiple Intra-species Variants of Human Zonadhesin.";	SEQUENCE	291277 MW; 2253CC9F222D/C45F CRC64;
RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	Query Match	Score 109; DB 4; Length 2689;
RL	-!- SIMILARITY: CONTAINS 3 MAM DOMAINS.	Best Local Similarity	35.3%; Pred. No. 1.4e-05;
CC	EMBL; AF333976; AAK01432_1; -.	Matches	24; Conservative 11; Mismatches 13; Indels 20; Gaps 4;
DR	HSSP; P56682; ICSV.	Qy	11 KCPNSNEIFSRC-----DGRCORFCNVVPKPLCIKICAGCVCRLGVLRNKKV 59
DR	InterPro; IPR00561; EGF-like.	Db	2210 ECPAYSSYTNCPLSPSCPSWCWLDGRCE--GAKVP---SACAEGCICQPGYVLSEDK- 2260
DR	InterPro; IPR001998; MAM_domain.	Qy	60 CYPRSKCG 67
DR	InterPro; IPR002965; P_rich_extensn.	Db	2261 CYPRSQCG 2268
DR	InterPro; IPR003328; TILA_Cysrich.	RESULT 15	
DR	InterPro; IPR00019; TIL_Cysrich.	ID	Q9BZ83 PRELIMINARY;
DR	InterPro; IPR001846; VWF_D.	AC	09BZ83;
PFam	PF00629; MAM; 3.	DT	01-JUN-2001 (TREMBLrel 17, Created)
PFam	PF01826; TIL; 5.	DT	01-JUN-2001 (TREMBLrel 17, Last sequence update)
PFam	PF02345; TILA; 4.	DT	01-JUN-2002 (TREMBLrel 21, Last annotation update)
PFam	PF00034; vwd; 4.	DE	Zonadhesin variant 6.
DR	PRINTS; PRO1217; PRICHEXTNSN.	GN	ZAN.
DR	SMART; SM00137; MAM; 3.	OS	Homo sapiens (Human).
SMART	SM00216; VWD; 4.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	PROSITE; PS01186; EGF_2; UNKNOWN_3.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DR	PROSITE; PS00740; MAM_1; 1.	NCBI_TaxID=9606;	
DR	PROSITE; PS50060; MAM_2; 3.	RN	[1]
KW	GLycoprotein;	RP	SEQUENCE FROM N.A.
SEQUENCE	291353 MW; 7E12C3343BF0408C CRC64;	RC	
Query Match	27.9%; Score 109; DB 4; Length 2689;	RA	TISSUE=TESTIS;
Best Local Similarity	35.3%; Pred. No. 1.4e-05;	RT	Cheung T.L., Wassler M.J., Cornwall G.A., Hardy D.M.; "Multiple Intra-species Variants of Human Zonadhesin."
Matches	24; Conservative 11; Mismatches 13; Indels 20; Gaps 4;	RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC	!-!- SIMILARITY: CONTAINS 3 MAM DOMAINS.	CC	-!- SIMILARITY: CONTAINS 3 MAM DOMAINS.
DR	AF332980; AAK01436_1; -.	DR	AF332980; AAK01436_1; -.
DR	HSSP; P56682; ICCV.	DR	InterPro; IPRO00561; EGF-like.
DR	InterPro; IPRO00998; MAM domain.	DR	InterPro; IPRO00998; MAM domain.
DR	InterPro; IPRO01665; P_rich_extensn.	DR	InterPro; IPRO01665; P_rich_extensn.
DR	InterPro; IPRO03328; TILA_Cysrich.	DR	InterPro; IPRO03328; TILA_Cysrich.
DR	PRINTS; PRO01217; PRICHEXTNSN.	DR	InterPro; IPRO01217; PRICHEXTNSN.
DR	SMART; SM00001; EGF_like; 1.	DR	SMART; SM00001; EGF_like; 1.
PFam	PF00629; MAM; 3.	DR	SMART; SM00216; VWD; 4.
PFam	PF01826; TIL; 4.	DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.
PFam	PF02345; TILA; 4.	DR	PROSITE; PS00024; EGF_2; UNKNOWN_4.
PFam	PF00094; vwd; 4.	DR	PROSITE; PS00186; MAM_1; 1.
DR	PRINTER; PRO01217; PRICHEXTNSN.	DR	PROSITE; PS00740; MAM_2; 3.
DR	SMART; SM00216; VWD; 4.	KW	GLycoprotein;
SEQUENCE	295506 MW; 142E9GBF3D404EC3 CRC64;	Qy	11 KCPNSNEIFSRC-----DGRCORFCNVVPKPLCIKICAGCVCRLGVLRNKKV 59
Query Match	27.9%; Score 109; DB 4; Length 2721;	Db	2210 ECPAYSSYTNCPLSPSCPSWCWLDGRCE--GAKVP---SACAEGCICQPGYVLSEDK- 2260
Best Local Similarity	35.3%; Pred. No. 1.4e-05;	Matches	24; Conservative 11; Mismatches 13; Indels 20; Gaps 4;
CC	!-!- SIMILARITY: CONTAINS 3 MAM DOMAINS.	Qy	11 KCPNSNEIFSRC-----DGRCORFCNVVPKPLCIKICAGCVCRLGVLRNKKV 59
DR	"Genomic Basis of Inter- and Intra-species Variation in Zonadhesin Domains Structure."; to the EMBL/GenBank/DBJ databases.	Db	2261 CYPRSQCG 2268
RL	Zonadhesin splice variant 2.	Qy	60 CYPRSKCG 67
ZN	ZAN.	Db	2261 CYPRSQCG 2268
OS	Homo sapiens (Human).	RESULT 14	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	ID	Q96L85 PRELIMINARY;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AC	096L85; 19, Created
OX	NCBI_TaxID=9606;	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
RN	SEQUENCE FROM N.A.	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
RA	Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.; "Genomic Basis of Inter- and Intra-species Variation in Zonadhesin Domains Structure."; to the EMBL/GenBank/DBJ databases.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
RT	Dominated (JUL-2001) to the EMBL/GenBank/DBJ databases.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR	!-!- SIMILARITY: CONTAINS 3 MAM DOMAINS.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR	EMBL; AY046055; AAL04415_1; -.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR	InterPro; IPRO00561; EGF-like.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR	InterPro; IPRO00938; MAM_domain.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR	InterPro; IPRO03328; TILA_Cysrich.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR	InterPro; IPRO02919; TILA_Cysrich.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Pfam	PF00629; MAM; 3.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Pfam	PF01826; TIL; 5.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Pfam	PF02345; TILA; 4.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
PROSITE	.PS00094; vwd; 4.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
PROSITE	.PS01186; MAM_1; 1.	DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
KW	GLycoprotein;	SEQUENCE	2721 AA; 295506 MW; 142E9GBF3D404EC3 CRC64;

Wed Feb 26 15:12:39 2003

us-09-506-978-1.open.rspt

Page 7

Search completed: February 26, 2003, 15:05:43
Job time : 31 secs



RESULT 1
 ABB08330
 ID ABB08330 standard; protein; 67 AA.
 XX
 AC ABB08330;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Bee venom protein Api m 6.01.
 XX
 KW Bee venom; isoform; immunosuppressant; vaccine; Api m 6; immune response;
 KW bee venom hypersensitivity; antibody; protein purification; Api m 6.01;
 KW immunotherapy; allergen

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

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3

New bee venom polypeptides, useful for modulating immune responses e.g. in individual hypersensitivity to the venom and for identifying individual at risk for bee venom hypersensitivity

Dossarin

result	No.	Score	Query Match	Length	DB	ID	Description
	1	391	100.0	67	23	ABP08330	Bee venom protein
	2	391	100.0	69	23	ABP08331	Bee venom protein
	3	391	100.0	71	23	ABP08332	Bee venom protein
	4	391	100.0	73	23	ABP08333	Bee venom protein
	5	391	100.0	92	21	AAE69209	Amino acid sequence
	6	108	27.6	3843	22	ABP1529	drosophila melanogaster
	7	107.5	27.5	2476	20	AAE67738	Pig p105 zona pellicle
	8	106.5	27.2	2594	16	AAW14748	IgG-IC binding protein
	9	106.5	27.2	2957	22	ABE22214	Novel human diagnosis
	10	106.5	27.2	2957	22	AAAE7474	IgG-IC binding protein

Example 2; Page 26; 32pp; English.

The present sequence is that of one the four isoforms of Api m 6, designated Api m 6.02. All four isoforms share a common central amino acid sequence shared by all four isoforms (see ABB08330, ABB08332 and ABB08333). The specification describes a substantially pure polypeptide, Api m 6, derived from bee venom and found in four isoforms. The proteins of the invention have immunosuppressant activity and may form the basis of a vaccine. Api m 6 is useful for modulating an immune response, i.e. as an allergen for immunotherapy. The protein is useful for identifying an individual at risk for bee venom hypersensitivity. The method comprises administering Api m 6 to the individual and measuring an immune response raised, where a detectable immune response indicates that the individual is at risk for bee venom hypersensitivity. Antibodies specific for Abi m 6 are useful for purifying the protein.

RESULT 2	
BB08311	ABB08311 standard; protein; 69 AA.
BB08311	ABB08311;
	18-JUN-2002 (first entry)
	Bee venom protein Api m 6.02.
	Bee venom; isoform; immunosuppressant; vaccine; Api m 6; immune response; bee venom hypersensitivity; antibody; protein purification; Ani m 6.02; bee venom; isoform; immunosuppressant; vaccine; Api m 6; immune response; bee venom hypersensitivity; antibody; protein purification; Api m 6.03; bee venom; isoform; immunosuppressant; vaccine; Api m 6; immune response; bee venom hypersensitivity; antibody; protein purification; Api m 6.03; immunotherapy; allergen.

7	immunotherapy; allergen.		
	Apis sp.	OS XX PN WO200188085-A2.	Apis sp.
	Key	Location/Qualifiers	
	Misc-difference 68		
		/label= Pro, Leu	
	Misc-difference 69		
		/label= Pro, Leu	
	WO200188085-A2.		
	22-NOV-2001.		
	16-FEB-2001; 2001WO-IB01736.		
		PP XX PR XX PA XX PI XX DR XX	
		(ECOL-) ECOLE POLYTECHNIQUE FEDERALE LAUSANNE. Spertini F;	

P1 New bee venom polypeptides, useful for modulating immune responses e.g.
PT in individual hypersensitivity to the venom and for identifying
PT individual at risk for bee venom hypersensitivity -
XX
PS Example 2; Page 26; 32pp; English.
XX
CC The present sequence is that of one the four isoforms of Apim 6,
CC designated Apim 6.03. All four isoforms share a common central amino
CC acid sequence shared by all four isoforms (see ABB08330, ABB08331 and
CC ABB08333). The specification describes a substantially pure polypeptide,
CC Apim 6, derived from bee venom and found in four isoforms. The proteins
CC of the invention have immunosuppressant activity and may form the basis
CC of a vaccine. Apim 6 is useful for modulating an immune response, i.e.
CC .
XX
PWI; 2002-082988/11.
CC New bee venom polypeptides, useful for modulating immune responses e.g.
CC in individual hypersensitivity to the venom and for identifying
CC individual at risk for bee venom hypersensitivity -
CC
PS Example 2; Page 26; 32pp; English.
XX

CC as an allergen for immunotherapy. The protein is useful for identifying
 CC an individual at risk for bee venom hypersensitivity. The method
 CC comprises administering Api m 6 to the individual and measuring an immune
 CC response raised, where a detectable immune response indicates that the
 CC individual is at risk for bee venom hypersensitivity. Antibodies specific
 CC for Api m 6 are useful for purifying the protein.

XX SQ Sequence 71 AA;
 Query Match 100.0%; Score 391; DB 23; Length 71;
 Best Local Similarity 100.0%; Pred. No. 8.4e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFGGGIAGRGKCPNSNIFSRCDGRCORFCPNVPKPLCIRKICAPGCCVRLGYLRNKKYC 60
 Db 5 GFGGGIAGRGKCPNSNIFSRCDGRCORFCPNVPKPLCIRKICAPGCCVRLGYLRNKKYC 64
 QY 61 VPRSKCG 67
 Db 65 VPRSKCG 71

RESULT 4

ABB08333 standard; protein: 73 AA.
 XX AC ABB08333;
 XX DT 18-JUN-2002 (first entry)

XX DE Bee venom protein Api m 6.04.
 XX Bee venom; isoform: immunosuppressant; vaccine; Api m 6; immune response;
 KW bee venom hypersensitivity; antibody; protein purification; Api m 6.04;
 KW immunotherapy; allergen.
 XX OS Apis sp.
 XX FH Key
 FT Misc-difference 72
 FT Misc-difference 73
 XX PN WO200188085-A2.

XX 22-NOV-2001.
 XX PD 16-FEB-2001; 2001WO-1B01736.
 XX PR 18-FEB-2000; 2000US-0506978.

XX PA (ECOL-) ECOLE POLYTECHNIQUE FEDERALE LAUSANNE.
 XX PI Spertini F;
 XX WPI; 2002-082988/11.

XX New bee venom polypeptides, useful for modulating immune responses e.g.,
 PT in individual hypersensitive to the venom and for identifying
 PT individual at risk for bee venom hypersensitivity -
 XX Example 2; Page 26; 32pp; English.
 XX DR

CC The present sequence is that of one the four isoforms of Api m 6,
 CC designated Api m 6.04. All four isoforms share a common central amino
 CC acid sequence shared by all four isoforms (see ABB08330, ABB08331 and
 CC ABB08332). The specification describes a substantially pure polypeptide,
 CC Api m 6, derived from bee venom and found in four isoforms. The proteins
 CC of the invention have immunosuppressant activity and may form the basis
 CC of a vaccine. Api m 6 is useful for modulating an immune response, i.e.
 CC as an allergen for immunotherapy. The protein is useful for identifying
 CC an individual at risk for bee venom hypersensitivity. The method

comprises administering Api m 6 to the individual and measuring an immune
 response raised, where a detectable immune response indicates that the
 individual is at risk for bee venom hypersensitivity. Antibodies specific
 for Api m 6 are useful for purifying the protein.

XX SQ Sequence 73 AA;

Query Match 100.0%; Score 391; DB 23; Length 73;

Best Local Similarity 100.0%; Pred. No. 8.6e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFGGLGGRKCPNSNIFSRCDGRCORFCPNVPKPLCIRKICAPGCCVRLGYLRNKKYC 60
 Db 5 GGFGGLGGRKCPNSNIFSRCDGRCORFCPNVPKPLCIRKICAPGCCVRLGYLRNKKYC 64

QY 61 VPRSKCG 67
 Db 65 VPRSKCG 71

RESULT 5

AY66209
 ID AAY66209 standard; protein: 92 AA.

XX AC AAY66209;
 XX DT 30-MAY-2000 (first entry)

XX DE Amino acid sequence of honey bee venom Px3.101 protein.
 XX Protein Px3.101; honey bee; venom; interleukin-8; receptor;
 KW CXCR1; CXCR2; cyclooxygenase; lipoxygenase; phospholipase; protease;
 KW inflammatory disease; gene therapy; cancer; autoimmune disease; pain;
 KW chemokine imbalance; rheumatoid arthritis; multiple sclerosis; pain;
 KW psoriasis; systemic lupus erythematosus; Crohn's disease; vasculitis;
 KW scleroderma; metastatic cancer; Alzheimer's disease; wound healing;
 KW aging process; antigen.

XX OS Apis mellifera.

XX FH Key
 FT Pept.de
 FT Region
 FT /note= "this region contains 5 GGX repeats"
 XX PN GB2341389-A.
 XX PD 15-MAR-2000.
 XX PF 13-SEP-1999;
 XX PR 14-SEP-1998;
 XX PA (PANP-) PAN PACIFIC PHARM INC.
 XX PI Chi X, Lu Y;
 XX DR 2000-185368/17.
 XX DR N-PSDB; A4261247.

XX Isolated nucleic acids encoding the bee venom protein Px3.101 useful
 PT for treating autoimmune and inflammatory disorders such as rheumatoid
 PT arthritis -
 XX WPI: 2000-185368/17.
 XX PS Claim 2; Fig 3A-B; 83pp; English.
 XX PT The present sequence represents the protein Px3.101, which is a honey
 CC bee venom isolated *Apis mellifera*. Px3.101 inhibits the binding of
 CC interleukin-8 (IL-8) to its receptor (e.g. CXCR1 and CXCR2) and
 CC inhibits a variety of enzymes (e.g. cyclooxygenases, lipoxygenases,
 CC phospholipases and proteases) associated with inflammatory diseases.
 CC The nucleic acids may be used for the recombinant production of

PX3.101 proteins either in vivo (as part of a gene therapy protocol) or in vitro (as a fermenter culture). The nucleic acids may also be used as probes to identify similar sequences in samples. The PX3.101 protein may be used for the treatment of inflammatory diseases, cancers, autoimmune diseases, pain and/or diseases associated with chemokine (especially IL-8) imbalances such as rheumatoid arthritis, multiple sclerosis, psoriasis, systemic lupus erythematosus ('SLE'), Crohn's disease, vasculitis, scleroderma, metastatic cancer and Alzheimer's disease in humans. It is also disclosed that the proteins may be used to accelerate wound healing, reduce several aging processes and protect against ultraviolet light. The proteins may also be used as antigens in the production of antibodies specific for PX3.101. The antibodies may be used as diagnostic agents to detect PX3.101 protein in samples and to down regulate PX3.101 activity.

Sequence 92 AA;

Query Match 100.0%; Score 391; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-31; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 0; IDles 0; Gaps 0;

Qy 1 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 60

Db 26 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 85

Qy 61 VPRSKCG 67

Db 86 VPRSKCG 92

Query Match 100.0%; Score 391; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-31; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 0; IDles 0; Gaps 0;

Qy 1 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 60

Db 26 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 85

Qy 61 VPRSKCG 67

Db 86 VPRSKCG 92

Query Match 100.0%; Score 391; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-31; Indels 0; Gaps 0;

Qy 1 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 60

Db 26 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 85

Qy 61 VPRSKCG 67

Db 86 VPRSKCG 92

Query Match 100.0%; Score 391; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-31; Indels 0; Gaps 0;

Qy 1 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 60

Db 26 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 85

Qy 61 VPRSKCG 67

Db 86 VPRSKCG 92

Query Match 100.0%; Score 391; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-31; Indels 0; Gaps 0;

Qy 1 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 60

Db 26 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 85

Qy 61 VPRSKCG 67

Db 86 VPRSKCG 92

Query Match 100.0%; Score 391; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-31; Indels 0; Gaps 0;

Qy 1 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 60

Db 26 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 85

Qy 61 VPRSKCG 67

Db 86 VPRSKCG 92

Query Match 100.0%; Score 391; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-31; Indels 0; Gaps 0;

Qy 1 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 60

Db 26 GGFFGLGGRKCPNSEIFRCDGRCQRFCPNVPKPCLIKICAPGCYVRLGTLRNKKVC 85

Qy 61 VPRSKCG 67

Db 1507 PLSQCG 1512

CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB7737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_Pct_sequences.
XX

SQ Sequence 3843 AA;
Query Match 27.6%; Score 108; DB 22; Length 3843;
Best Local Similarity 33.9%; Pred. No. 0.035; IDles 0; Gaps 0;
Matches 19; Conservative 7; Mismatches 30; Indels 0;
ID AAW67738 standard; Protein: 2476 AA.
XX
AAW67738:
AC XX
DT 16-MAR-1999 (first entry)
XX
DE Pig p105 zona pellucida-binding protein.
XX
KW Pig; porcine; sperm; egg-binding protein; zona pellucida; contraception;
KW fertillisation.
XX
OS Sus scrofa.
XX
PN US5851817-A.
XX
US5851817-A.
XX
PD 22-DEC-1998.
XX
PF 19-JUL-1994; 94US-0276967.
XX
PR 19-JUL-1994; 94US-0276967.
XX
(TEXA) UNIV TEXAS SYSTEM.
PA
XX
PI Garbers DL, Hardy DM;
XX
WPI: 1999-080410/07.
DR N-PSDB; AA81446.
XX
DNA encoding porcine sperm protein - useful for
PT producing recombinant protein
XX
PS Claim 1; Fig 8A-B; 47pp; English.
XX
This sequence represents a pig sperm egg-binding protein designated
CC protein p105. Porcine sperm proteins which bind the zona pellucida in a
CC species-specific manner were isolated. Separation by gel electrophoresis
CC resulted in bands of proteins with molecular weights of 130, 150 and
CC 170 kD, under native conditions but bands of 105 and 45 kD were observed
CC when the proteins were separated under denaturing conditions. Compounds
CC which bind these proteins can be used for contraception or fertillisation.
XX
SQ Sequence 2476 AA;

Query Match 27.5%; Score 107.5; DB 20; Length 2476;
Best Local Similarity 33.3%; Pred. No. 0.027; IDles 17; Gaps 3;
Matches 22; Conservative 9; Mismatches 18; Indels 17;
ID AAW67738 standard; Protein: 2476 AA.
XX
AAW67738:
AC XX
DT 16-MAR-1999 (first entry)
XX
DE Pig p105 zona pellucida-binding protein.
XX
KW Pig; porcine; sperm; egg-binding protein; zona pellucida; contraception;
KW fertillisation.
XX
OS Sus scrofa.
XX
PN US5851817-A.
XX
US5851817-A.
XX
PD 22-DEC-1998.
XX
PF 19-JUL-1994; 94US-0276967.
XX
PR 19-JUL-1994; 94US-0276967.
XX
(TEXA) UNIV TEXAS SYSTEM.
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XX
PI Garbers DL, Hardy DM;
XX
WPI: 1999-080410/07.
DR N-PSDB; AA81446.
XX
DNA encoding porcine sperm protein - useful for
PT producing recombinant protein
XX
PS Claim 1; Fig 8A-B; 47pp; English.
XX
This sequence represents a pig sperm egg-binding protein designated
CC protein p105. Porcine sperm proteins which bind the zona pellucida in a
CC species-specific manner were isolated. Separation by gel electrophoresis
CC resulted in bands of proteins with molecular weights of 130, 150 and
CC 170 kD, under native conditions but bands of 105 and 45 kD were observed
CC when the proteins were separated under denaturing conditions. Compounds
CC which bind these proteins can be used for contraception or fertillisation.
XX
SQ Sequence 2476 AA;

Query Match 27.5%; Score 107.5; DB 20; Length 2476;
Best Local Similarity 33.3%; Pred. No. 0.027; IDles 17; Gaps 3;
Matches 22; Conservative 9; Mismatches 18; Indels 17;
ID AAW67738 standard; Protein: 2476 AA.
XX
AAW67738:
AC XX
DT 16-MAR-1999 (first entry)
XX
DE Pig p105 zona pellucida-binding protein.
XX
KW Pig; porcine; sperm; egg-binding protein; zona pellucida; contraception;
KW fertillisation.
XX
OS Sus scrofa.
XX
PN US5851817-A.
XX
US5851817-A.
XX
PD 22-DEC-1998.
XX
PF 19-JUL-1994; 94US-0276967.
XX
PR 19-JUL-1994; 94US-0276967.
XX
(TEXA) UNIV TEXAS SYSTEM.
PA
XX
PI Garbers DL, Hardy DM;
XX
WPI: 1999-080410/07.
DR N-PSDB; AA81446.
XX
DNA encoding porcine sperm protein - useful for
PT producing recombinant protein
XX
PS Claim 1; Fig 8A-B; 47pp; English.
XX
This sequence represents a pig sperm egg-binding protein designated
CC protein p105. Porcine sperm proteins which bind the zona pellucida in a
CC species-specific manner were isolated. Separation by gel electrophoresis
CC resulted in bands of proteins with molecular weights of 130, 150 and
CC 170 kD, under native conditions but bands of 105 and 45 kD were observed
CC when the proteins were separated under denaturing conditions. Compounds
CC which bind these proteins can be used for contraception or fertillisation.
XX
SQ Sequence 2476 AA;

Query Match 27.5%; Score 107.5; DB 20; Length 2476;
Best Local Similarity 33.3%; Pred. No. 0.027; IDles 17; Gaps 3;
Matches 22; Conservative 9; Mismatches 18; Indels 17;
ID AAW67738 standard; Protein: 2476 AA.
XX
AAW67738:
AC XX
DT 16-MAR-1999 (first entry)
XX
DE Pig p105 zona pellucida-binding protein.
XX
KW Pig; porcine; sperm; egg-binding protein; zona pellucida; contraception;
KW fertillisation.
XX
OS Sus scrofa.
XX
PN US5851817-A.
XX
US5851817-A.
XX
PD 22-DEC-1998.
XX
PF 19-JUL-1994; 94US-0276967.
XX
PR 19-JUL-1994; 94US-0276967.
XX
(TEXA) UNIV TEXAS SYSTEM.
PA
XX
PI Garbers DL, Hardy DM;
XX
WPI: 1999-080410/07.
DR N-PSDB; AA81446.
XX
DNA encoding porcine sperm protein - useful for
PT producing recombinant protein
XX
PS Claim 1; Fig 8A-B; 47pp; English.
XX
This sequence represents a pig sperm egg-binding protein designated
CC protein p105. Porcine sperm proteins which bind the zona pellucida in a
CC species-specific manner were isolated. Separation by gel electrophoresis
CC resulted in bands of proteins with molecular weights of 130, 150 and
CC 170 kD, under native conditions but bands of 105 and 45 kD were observed
CC when the proteins were separated under denaturing conditions. Compounds
CC which bind these proteins can be used for contraception or fertillisation.
XX
SQ Sequence 2476 AA;

CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB7737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_Pct_sequences.
XX

SQ Sequence 3843 AA;
Query Match 27.6%; Score 108; DB 22; Length 3843;
Best Local Similarity 33.9%; Pred. No. 0.035; IDles 0; Gaps 0;
Matches 19; Conservative 7; Mismatches 30; Indels 0;
ID AAW67738 standard; Protein: 2476 AA.
XX
AAW67738:
AC XX
DT 16-MAR-1999 (first entry)
XX
DE Pig p105 zona pellucida-binding protein.
XX
KW Pig; porcine; sperm; egg-binding protein; zona pellucida; contraception;
KW fertillisation.
XX
OS Sus scrofa.
XX
PN US5851817-A.
XX
US5851817-A.
XX
PD 22-DEC-1998.
XX
PF 19-JUL-1994; 94US-0276967.
XX
PR 19-JUL-1994; 94US-0276967.
XX
(TEXA) UNIV TEXAS SYSTEM.
PA
XX
PI Garbers DL, Hardy DM;
XX
WPI: 1999-080410/07.
DR N-PSDB; AA81446.
XX
DNA encoding porcine sperm protein - useful for
PT producing recombinant protein
XX
PS Claim 1; Fig 8A-B; 47pp; English.
XX
This sequence represents a pig sperm egg-binding protein designated
CC protein p105. Porcine sperm proteins which bind the zona pellucida in a
CC species-specific manner were isolated. Separation by gel electrophoresis
CC resulted in bands of proteins with molecular weights of 130, 150 and
CC 170 kD, under native conditions but bands of 105 and 45 kD were observed
CC when the proteins were separated under denaturing conditions. Compounds
CC which bind these proteins can be used for contraception or fertillisation.
XX
SQ Sequence 2476 AA;

CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB7737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_Pct_sequences.
XX

SQ Sequence 3843 AA;
Query Match 27.6%; Score 108; DB 22; Length 3843;
Best Local Similarity 33.9%; Pred. No. 0.035; IDles 0; Gaps 0;
Matches 19; Conservative 7; Mismatches 30; Indels 0;
ID AAW67738 standard; Protein: 2476 AA.
XX
AAW67738:
AC XX
DT 16-MAR-1999 (first entry)
XX
DE Pig p105 zona pellucida-binding protein.
XX
KW Pig; porcine; sperm; egg-binding protein; zona pellucida; contraception;
KW fertillisation.
XX
OS Sus scrofa.
XX
PN US5851817-A.
XX
US5851817-A.
XX
PD 22-DEC-1998.
XX
PF 19-JUL-1994; 94US-0276967.
XX
PR 19-JUL-1994; 94US-0276967.
XX
(TEXA) UNIV TEXAS SYSTEM.
PA
XX
PI Garbers DL, Hardy DM;
XX
WPI: 1999-080410/07.
DR N-PSDB; AA81446.
XX
DNA encoding porcine sperm protein - useful for
PT producing recombinant protein
XX
PS Claim 1; Fig 8A-B; 47pp; English.
XX
This sequence represents a pig sperm egg-binding protein designated
CC protein p105. Porcine sperm proteins which bind the zona pellucida in a
CC species-specific manner were isolated. Separation by gel electrophoresis
CC resulted in bands of proteins with molecular weights of 130, 150 and
CC 170 kD, under native conditions but bands of 105 and 45 kD were observed
CC when the proteins were separated under denaturing conditions. Compounds
CC which bind these proteins can be used for contraception or fertillisation.
XX
SQ Sequence 2476 AA;

RESULT 8
 AAW14718
 ID AAW14748 standard; Protein; 2594 AA.
 XX
 AC AAW14748;
 XX DT 13-MAY-1997 (first entry)
 XX DE IgG-Fc binding protein encoded by 7.8 kb fragment of pNV11-ST.
 XX PR Fragment 13; pNV11-ST; IgG-Fc binding protein; immunoglobulin; K17;
 KW human; colonic epithelium; monoclonal antibody; K9; probe.
 XX OS Homo sapiens.
 XX PN WO200175057-A2;
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-054217.
 XX PR 23-AUG-2000; 2000US-0649167.
 PA (HYSEQ) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 XX DR N-PSDB; AAS86401.
 PS Claim 20: SEQ ID No 52573; 103pp; English.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX PT The invention relates to isolated polynucleotide (I) and
 PT polypeptide (II) sequences. (I) is useful as hybridisation probes,
 PT polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 PT and gene mapping, and in recombinant production of (II). The
 PT polynucleotides are also used in diagnostics as expressed sequence tags
 PT for identifying expressed genes. (I) is useful in gene therapy techniques
 PT to restore normal activity of (II) or to treat disease states involving
 PT (II). (II) is useful for generating antibodies against it, detecting or
 PT quantitating a polypeptide in tissue, as molecular weight markers and as
 PT a food supplement. (II) and its binding partners are useful for treating
 PT disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010 ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 2957 AA;

Query Match 27.2%; Score 106.5; DB 16; Length 2594;
 Best Local Similarity 36.8%; Pred. No. 0.035;
 Matches 21; Conservative 6; Mismatches 29; Indels 1; Gaps 1;

Qy 11 KCPSENIEIFSRCDGRQRFFCPNVPKPLCIKIKAPGCYGRGLYLRNKKVCPRSKCG 67
 Db 1531 ECPPNSHYELCADCOTSLGCSALSAPPQCDGCAEGQCDSGFLYN-GOACVP1QQCG 1586

RESULT 9
 ABG22214
 ID ABG22214 standard; Protein; 2957 AA.
 XX AC ABG22214;
 XX DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #22205.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensics;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.

Query Match 21; Conservative 6; Mismatches 29; Indels 1; Gaps 1;
 Best Local Similarity 36.8%; Pred. No. 0.039;
 Matches 21; Conservative 6; Mismatches 29; Indels 1; Gaps 1;
 Qy 11 KCPSENIEIFSRCDGRQRFFCPNVPKPLCIKIKAPGCYGRGLYLRNKKVCPRSKCG 67
 Db 1623 ECPPNSHYELCADCOTSLGCSALSAPPQCDGCAEGQCDSGFLYN-GOACVP1QQCG 1678

RESULT 10
 AAW14749
 ID AAW14749 standard; Protein; 5405 AA.
 XX AC AAW14749;
 XX DT 13-MAY-1997 (first entry)
 DE IgG-Fc binding protein.
 XX KW Fragment 13; pNV11-ST; IgG-Fc binding protein; immunoglobulin; K17;
 KW human; colonic epithelium; monoclonal antibody; K9; probe.
 OS Homo sapiens.

PN WO9522057-A1.
 XX PD 12-OCT-1995.
 XX PF 03-APR-1995; 95WO-JP00638.
 XX PR 30-MAR-1995; 95JP-0109927.
 PR 01-APR-1994; 94JP-0129487.
 PR 24-AUG-1994; 94JP-0222547.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Harada N, Morikawa M;
 XX WPI; 1995-358632/46.
 DR N-PSPDB; AAT63074.
 XX DNA derived from colonic epithelium encoding IgG-Fc binding protein
 - used in the mapping and analysis of IgG-Fc binding protein mRNA
 XX PS Claim 3; Page 86-113; 132pp; Japanese.
 XX This sequence represents the IgG-Fc binding protein of human colonic
 epithelium. This sequence was isolated using the sequence given in
 AAW14748. mRNA isolated from human colonic epithelial tissue was used
 to prepare a cDNA library. This was screened using monoclonal
 antibodies K9 and K17 which bind to the large and small components of the
 binding protein. Active clones, see also AAT63077-81, were used to
 derive probes for screening a second DNA library from human colonic
 epithelial tissue.
 XX Sequence 5405 AA;
 Query Match 27 2%; Score 106 5; DB 16; Length 5405;
 Best Local Similarity 36.8%; Pred. No. 0.066;
 Matches 21; Conservative 6; Mismatches 29; Indels 1; Gaps 1;
 Qy 11 KCPNSNEIFSRCDGRQRFQVPLKICAPGCVRLRNKKVCPRSKCG 67
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1531 ECPPNSHYECLADTCSLGCCSALSAPPQCDGSFLYNGQACVPIQQCG 1586
 Sequence 5405 AA;

PN WO9522057-A1.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE) HYSEQ INC.
 XX DR Drmanac RT, Liu C, Tang YT;
 DR WPI; 2001-639362/73.
 XX DR N-PSPDB; AAS86402.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX PS Claim 20; SEQ ID NO 52575; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences, (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products based on DNA and
 CC amino acid sequences. ABG0010-ABG3037 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftt.wipo.int/pub/published_pct_sequences.
 XX Sequence 7337 AA;
 SQ

Query Match 26 0%; Score 101.5; DB 22; Length 7337;
 Best Local Similarity 31.6%; Pred. No. 0.27;
 Matches 18; Conservative 10; Mismatches 28; Indels 1; Gaps 1;
 Qy 11 KCPNSNEIFSRCDGRQRFQVPLKICAPGCVRLRNKKVCPRSKCG 67
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 5181 QCRAHSHYELCQDPSGPSCPSLSAPEGCCSACREGCVCDAGEFVL-GDTCVPYGGCG 5236

RESULT 1.2
 ABG22215
 ID ABG22215 standard; Protein; 735 AA.
 XX AC ABG22215;
 AC ABG22215;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #22206.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WC000175067-A2.
 PD 11-OCT-2001.
 XX XX 30-MAR-2001; 2001WO-US08631.
 PF XX PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE) HYSEQ INC.
 XX DR Drmanac RT, Liu C, Tang YT;
 DR WPI; 2001-639362/73.
 XX DR N-PSPDB; AAS86402.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations

XX	Sequence	735 AA;
SQ	Query Match	25.7%; Score 100.5; DB 22; Length 735;
	Best Local Similarity	31.6%; Pred. No. 0.046;
	Matches 18; Conservative	10; Mismatches 28; Indels 1; Gap
QY	11 KCPSENEIFSRCDGRQRQFCPNNVPKPLC1KICAPSCVCRUGYLRNKKVCPRSKG 67	
Ddb	68 QCPAHSHYELCGDSCPVCPSLSAPEGCESACRESCVCDAGFVL5-GDTCPVGQCG 123	
	RESULT 13	
	AAV30432	
ID	AAV30432 standard	Protein; 84 AA.
XX		
AC	AAV30432;	
XX		
	15-NOV-1999 (first entry)	
DT	XX	Mature nematode extracted anticoagulant protein AcaNAPC2.
DE	XX	
KW	XX	Nematode extracted anticoagulant protein; NAP; anticoagulant;
KW	XX	serine protease inhibitor; NAP domain; factor VIIa/TF.
OS	XX	Ancylostoma caninum.
XX	XX	
US5955204-A.		
XX		
21-SEP-1999.		
PPD		
XX		
19-APR-1996;	96US-0634641.	
IPN		
XX		
19-APR-1996;	96US-0634641.	
IPR		
18-OCT-1994;	94US-0326110.	
IPR		
05-JUN-1995;	95US-0461965.	
IPR		
05-JUN-1995;	95US-0463380.	
IPR		
05-JUN-1995;	95US-0463397.	
IPR		
05-JUN-1995;	95US-0463399.	
IPR		
17-OCT-1995;	95WO-US13231.	
XXX		
PA	(CORV-) CORVAS INT INC.	
PA		
XX		
Bergum PW, Ganssenans YGJ, Jespers LS, Laroche YR;		
Lauwereys MJ, Messens JHL, Moyie M, Stanssens PEH;		
Vlasuk GP;		
XXX		

Result No.	Score	Query	Match	Length	DB	ID	Description
1	106.5	27.2	5405	9	US-10-025-380-1116	-	Sequence 1116, Ap
2	106.5	27.2	5405	10	US-09-922-217-1116	-	Sequence 1116, Ap
3	98	25.1	2813	10	US-09-381-261A-1	-	Sequence 1, Appli
4	87.5	22.4	2813	10	US-09-986-900-2	-	Sequence 2, Appli
5	85	21.7	759	9	US-10-189-971-2	-	Sequence 22, Appli
6	85	21.7	1057	9	US-10-189-971-6	-	Sequence 6, Appli
7	85	21.7	1192	9	US-10-189-971-18	-	Sequence 18, Appli
8	85	21.7	1207	9	US-10-189-971-20	-	Sequence 20, Appli
9	85	21.7	1251	9	US-10-189-971-16	-	Sequence 16, Appli
10	85	21.7	1342	9	US-10-189-971-24	-	Sequence 24, Appli
11	85	21.7	1477	9	US-10-189-971-8	-	Sequence 8, Appli
12	85	21.7	1512	9	US-10-189-971-10	-	Sequence 10, Appli
13	85	21.7	1535	9	US-10-189-971-14	-	Sequence 14, Appli
14	85	21.7	1570	9	US-10-189-971-12	-	Sequence 12, Appli
15	85	21.7	1593	9	US-10-189-971-4	-	Sequence 4, Appli
16	85	21.7	1628	9	US-10-189-971-2	-	Sequence 2, Appli
17	83.5	21.4	355	10	US-09-826-212-14	-	Sequence 14, Appli
18	83.5	21.4	355	10	US-09-935-727-16	-	Sequence 16, Appli
19	82.5	21.1	469	10	US-09-925-301-1279	-	Sequence 1279, Ap

Title:	GenCore version 5.1.3	Copyright (c) 1993 - 2003 Compugen Ltd.	Sequence 46, App1
OM protein - protein search, using sw model			Sequence 54, App1
Run on:	February 26, 2003, 15:05:12 ; Search time 33 Seconds (without alignments)		Sequence 2, Appli
Perfect score:	76.587 Million cell updates/sec		Sequence 13, App1
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Scoring table:	BLOSUM62		Sequence 103, App
	Gapop 10.0 , Gapext 0.5		Sequence 120, App
Searched:	174566 seqs, 37721826 residues		Sequence 43, Appli
Total number of hits satisfying chosen parameters:	174566		Sequence 11, Appli
Minimum DB seq length: 0			Sequence 100, App
Maximum DB seq length: 2000000000			Sequence 124, App
Post-processing: Minimum Match 0%			Sequence 5, Appli
Maximum Match 100%			Sequence 60, App
Listing first 45 summaries			Sequence 6, Appli
Database :	Published_Applications_AA:*		Sequence 60, App
	1: /cgn2_6/piodata/2/pubpaa/us08 NEW_PUB_PEP:*		Sequence 1116, Application US-10025380
	2: /cgn2_6/piodata/2/pubpaa/pct* NEW_PUB_PEP:*		Publication No. US20020182191A1
	3: /cgn2_6/piodata/2/pubpaa/pc* NEW_PUB_PEP:*		GENERAL INFORMATION:
	4: /cgn2_6/piodata/2/pubpaa/us06_PUBCOMB_PEP:*		APPLICANT: Xu, Jianchun
	5: /cgn2_6/piodata/2/pubpaa/us07_PUBCOMB_PEP:*		APPLICANT: Lodes, Michael J.
	6: /cgn2_6/piodata/2/pubpaa/us07_PUBCOMB_PEP:*		APPLICANT: Sechrist, Heather
	7: /cgn2_6/piodata/2/pubpaa/pct* NEW_PUB_PEP:*		APPLICANT: Benson, Darin R.
	8: /cgn2_6/piodata/2/pubpaa/pc* NEW_PUB_PEP:*		APPLICANT: Meagher, Madeleine Joy
	9: /cgn2_6/piodata/2/pubpaa/us08_PUBCOMB_PEP:*		APPLICANT: Stolk, John A.
	10: /cgn2_6/piodata/2/pubpaa/us09_PUBCOMB_PEP:*		APPLICANT: Wang, Tongtong
	11: /cgn2_6/piodata/2/pubpaa/us10_PUBCOMB_PEP:*		APPLICANT: Jiang, Yuqiu
	12: /cgn2_6/piodata/2/pubpaa/us10_PUBCOMB_PEP:*		APPLICANT: Smith, Carole L.
	13: /cgn2_6/piodata/2/pubpaa/us60_NEW_PUB_PEP:*		APPLICANT: King, Gordon E.
	14: /cgn2_6/piodata/2/pubpaa/us60_PUBCOMB_PEP:*		APPLICANT: Wang, Aljun
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			APPLICANT: Clapper, Jonathan D.
SUMMARIES			APPLICANT: Skeiky, Yasir A. W.
			APPLICANT: Fanger, Gary R.
			APPLICANT: Vedick Thomas S.
			APPLICANT: Carter, Derrick
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			APPLICANT: Fanger, Gary R.
			APPLICANT: Vedick Thomas

RESULT 2
US-09-922-217-1116
; Sequence: 1116 Application US/09922217
; Patent No. US2000076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Sechrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Ajun
; APPLICANT: Clipper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: COMPOUNDS FOR COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 20121_471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1116
; LENGTH: 5405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-217-1116

Query Match Score 27.2%; Pred. No. 0.027; Length 5405;
Best Local Similarity 36.8%; Mismatches 29; Indels 1;
Matches 21; Conservative 6; Gaps 1;

Qy 11 KCPNSNEIFSRCDGRQRFQPCPNVPKPLCIKICAPGCVCRLGYLRNKKVCPRSKCG 67
Db 1531 ECPNPSHYELCADTCSLGCSALSAAPQCDGCAEGCOCDFLYNGQACVPIQQG 15846

RESULT 3
US-09-381-261A-1
; Sequence 1, Application US/09381261A
; Patent No. US2002012457A1
; GENERAL INFORMATION:
; APPLICANT: Loscalzo, Joseph
; APPLICANT: Inbal, Aida
; TITLE OF INVENTION: No. US20020123457A1el Anti-Platelet Agent
; CURRENT APPLICATION NUMBER: US/09/381,261A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: PICPUS98/06092
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/046,981
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-381-261A-1

Query Match Score 25.1%; Pred. No. 0.098; Length 2813;
Best Local Similarity 26.0%; Mismatches 27; Indels 14; Gaps 2;
Matches 19; Conservative 13; Gaps 1;

Qy 8 GRG-----KCPNSEIFSRCDGRQRFQPCPNVPKPLCIKICAPGCVCRLGYL 53
Db 635 GRGKRVANBEPGRCELNPKQGVYLOQSTPCNUTCRSLSYDEECNAECLFCFCGPGLY 694

Qy 54 RNKKVCPRSKCG 66
; :|||::|

RESULT 4
US-09-886-900-2
; Sequence 2, Application US/09886900
; Patent No. US2002137051A1
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J.
; APPLICANT: Yuzbasyan-Turkan, Vilma
; APPLICANT: Schall, William D.
; APPLICANT: Brewer, George J.
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: 5445 Corporate Drive
; CITY: Troy
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48098
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/886,900
; FILING DATE: 21-JUN-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/396,449
; FILING DATE: 18-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REFERENCE/DOCKET NUMBER: 2115-001226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 248-641-1600
; TELEFAX: 248-641-0270
; TELEX: 287637
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2813 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-886-900-2

Query Match Score 22.4%; Pred. No. 0.99; Length 2813;
Best Local Similarity 31.0%; Mismatches 29; Indels 1; Gaps 1;
Matches 18; Conservative 10; Gaps 1;

Qy 9 RGKCPNSNEIFSRCDGRQRFQPCPNVPKPLCIKICAPGCVCRLGYLRNKKVCPRSKCG 66
Db 292 RPACPAGMEYKECVSPCTRTQSLHVKEYCQEVCVDGSCSPEGQLDEGH-CVGSAC 348

RESULT 5
US-10-189-971-22
; Sequence 22, Application US/10189971
; Publication No. US20030028907A1
; GENERAL INFORMATION:
; APPLICANT: Walk, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030028907A1 Human Kielin-like Proteins and Polynucle
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-US-A
; CURRENT APPLICATION NUMBER: US/10/189,971
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949

PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 22
; LENGTH: 759
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-189-971-22

Query Match 21.7%; Score 85; DB 9; Length 759;
Best Local Similarity 30.6%; Pred. No. 0.55%;
Matches 19; Conservative 8; Mismatches 27; Indels 8; Gaps 4;

Qy 12 CPSNE--IFSRCDGRQRCRCPNV-VP---KPLCIKICAPGCCVCRIGYLRNKKVCPRS 64
Db 674 CPLERGFVFDECGPPCPRTCFNQHPLGELAAHCVRPCVPGCQCPAGLVEHEAH-CIPPE 732

Qy 65 KC 66
Db 733 AC 734

RESULT 6
US-10-189-971-6
; Sequence 6, Application US/10189971
; Publication No. US20030028907A1
; GENERAL INFORMATION:
; APPLICANT: Walké, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030028907A1 Human Kielin-like Proteins and Polynucleotides
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 1057
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-189-971-6

Query Match 21.7%; Score 85; DB 9; Length 1057;
Best Local Similarity 30.6%; Pred. No. 0.73%;
Matches 27; Indels 8; Gaps 4;

Qy 12 CPSNE--IFSRCDGRQRCRCPNV-VP---KPLCIKICAPGCCVCRIGYLRNKKVCPRS 64
Db 972 CPLERGFVFDECGPPCPRTCFNQHPLGELAAHCVRPCVPGCQCPAGLVEHEAH-CIPPE 1030

Qy 65 KC 66
Db 1031 AC 1032

RESULT 7
US-10-189-971-18
; Sequence 18, Application US/10189971
; Publication No. US20030028907A1
; GENERAL INFORMATION:
; APPLICANT: Walké, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030028907A1 Human Kielin-like Proteins and Polynucleotides
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA

Query Match 21.7%; Score 85; DB 9; Length 1192;
Best Local Similarity 30.6%; Pred. No. 0.52%;
Matches 19; Conservative 8; Mismatches 27; Indels 8; Gaps 4;

Qy 12 CPSNE--IFSRCDGRQRCRCPNV-VP---KPLCIKICAPGCCVCRIGYLRNKKVCPRS 64
Db 1107 CPLERGFVFDECGPPCPRTCFNQHPLGELAAHCVRPCVPGCQCPAGLVEHEAH-CIPPE 1180

Qy 65 KC 66
Db 1166 AC 1167

RESULT 8
US-10-189-971-20
; Sequence 20, Application US/10189971
; Publication No. US20030028907A1
; GENERAL INFORMATION:
; APPLICANT: Walké, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030028907A1 Human Kielin-like Proteins and Polynucleotides
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/10/189,971
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 20
LENGTH: 1.207
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-189-971-20

Query Match 21.7%; Score 85; DB 9; Length 1207;
Best Local Similarity 30.6%; Pred. No. 0.82%;
Matches 19; Conservative 8; Mismatches 27; Indels 8; Gaps 4;

Qy 12 CPSNE--IFSRCDGRQRCRCPNV-VP---KPLCIKICAPGCCVCRIGYLRNKKVCPRS 64
Db 1122 CPLERGFVFDECGPPCPRTCFNQHPLGELAAHCVRPCVPGCQCPAGLVEHEAH-CIPPE 1180

Qy 65 KC 66
Db 1181 AC 1182

RESULT 9
US-10-189-971-16
; Sequence 16, Application US/10189971
; Publication No. US20030028907A1
; GENERAL INFORMATION:
; APPLICANT: Walké, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030028907A1 Human Kielin-like Proteins and Polynucleotides
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA

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; TITLE OF INVENTION: No. US20030028907A1 Human Kielin-like Proteins and Polynucleot
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/189,971
; CURRENT FILING DATE: 2002-07-03
; PRIORITY NUMBER: US 60/302,949
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 16
; LENGTH: 1251
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-189-971-16

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Best Local Similarity 30.6%;  Pred. No. 0.85;  Gaps 4;
Matches 19;  Conservative 8;  Mismatches 27;  Indels 8;  Gaps 4;
Query Match          21.7%;  Score 85;  DB 9;  Length 1477;
Best Local Similarity 30.6%;  Pred. No. 0.98;  Gaps 4;
Matches 19;  Conservative 8;  Mismatches 27;  Indels 8;  Gaps 4;
; ORGANISM: homo sapiens
US-10-189-971-8

Qy      12 CPSNE--IFSRCDGRQRFCPNV--KPLCIKICAPGVCRIGYLRNKKVCPRS 64
Db      1166 CPLERGFVFDCEGPPCPRTCFNQHPLGEAAHCYRPCVPGCCPAGLVHEAH-CIPPE 1224
Qy      65 KC 66
Db      1225 AC 1226

RESULT 10
US-10-189-971-24
; Sequence 24, Application US/10189971
; Publication No. US20030028907A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; SCOVILLE, John
; ATTORNEY: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/189,971
; CURRENT FILING DATE: 2002-07-03
; PRIORITY NUMBER: US 60/302,949
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 24
; LENGTH: 1342
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-189-971-24

Query Match          21.7%;  Score 85;  DB 9;  Length 1342;
Best Local Similarity 30.6%;  Pred. No. 0.9;  Gaps 4;
Matches 19;  Conservative 8;  Mismatches 27;  Indels 8;  Gaps 4;
Query Match          21.7%;  Score 85;  DB 9;  Length 1512;
Best Local Similarity 30.6%;  Pred. No. 1;
Matches 19;  Conservative 8;  Mismatches 27;  Indels 8;  Gaps 4;
; ORGANISM: homo sapiens
US-10-189-971-10

Qy      12 CPSNE--IFSRCDGRQRFCPNV--KPLCIKICAPGVCRIGYLRNKKVCPRS 64
Db      1257 CPLERGFVFDCEGPPCPRTCFNQHPLGEAAHCYRPCVPGCCPAGLVHEAH-CIPPE 1315
Qy      65 KC 66
Db      1316 AC 1317

RESULT 11
US-10-189-971-8
; Sequence 8, Application US/10189971
; Publication No. US20030028907A1
; GENERAL INFORMATION:

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RESULT 15
Sequence 14, Application US/10189971
; PUBLICATION NO. US20030028907A1
; GENERAL INFORMATION:
; APPLICANT: Walk, D. Wade
; APPLICANT: Scoville, John C. Alexander Jr.
; TITLE OF INVENTION: No. US20030028907A1 Human Kielin-like Proteins and Polynucleotides
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/10/189,971
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO. 14
; LENGTH: 1535
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-189-971-14

Query Match 21.7%; Score 85; DB 9; Length 1535;
Best Local Similarity 30.6%; Pred. No. 1; Gaps 4;
Matches 19; Conservative 8; Mismatches 27; Indels 8; Gaps 4;

Query 12 CPSNE--IFSRCDGRCORFCPNV-VP---KPLCIKICAPGCCVRGLYLRNKKVCPRS 64
Db 1450 CPLERGFVFDCEGPPCPRTCFNQHIPLGELAAHCVRPCVPGCOCPAGLVEHEAH-CIPPE 1508

Qy 65 KC 66
Db 1509 AC 1510

RESULT 14
US-10-189-971-12
; Sequence 12, Application US/10189971
; PUBLICATION NO. US20030028907A1
; GENERAL INFORMATION:
; APPLICANT: Walk, D. Wade
; APPLICANT: Scoville, John C. Alexander Jr.
; TITLE OF INVENTION: No. US20030028907A1 Human Kielin-like Proteins and Polynucleotides
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0360-USA
; CURRENT APPLICATION NUMBER: US/10/189,971
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/302,949
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/315,634
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO. 12
; LENGTH: 1570
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-189-971-12

Query Match 21.7%; Score 85; DB 9; Length 1570;
Best Local Similarity 30.6%; Pred. No. 1; Gaps 4;
Matches 19; Conservative 8; Mismatches 27; Indels 8; Gaps 4;

Query 12 CPSNE--IFSRCDGRCORFCPNV-VP---KPLCIKICAPGCCVRGLYLRNKKVCPRS 64
Db 1485 CPLERGFVFDCEGPPCPRTCFNQHIPLGELAAHCVRPCVPGCOCPAGLVEHEAH-CIPPE 1543

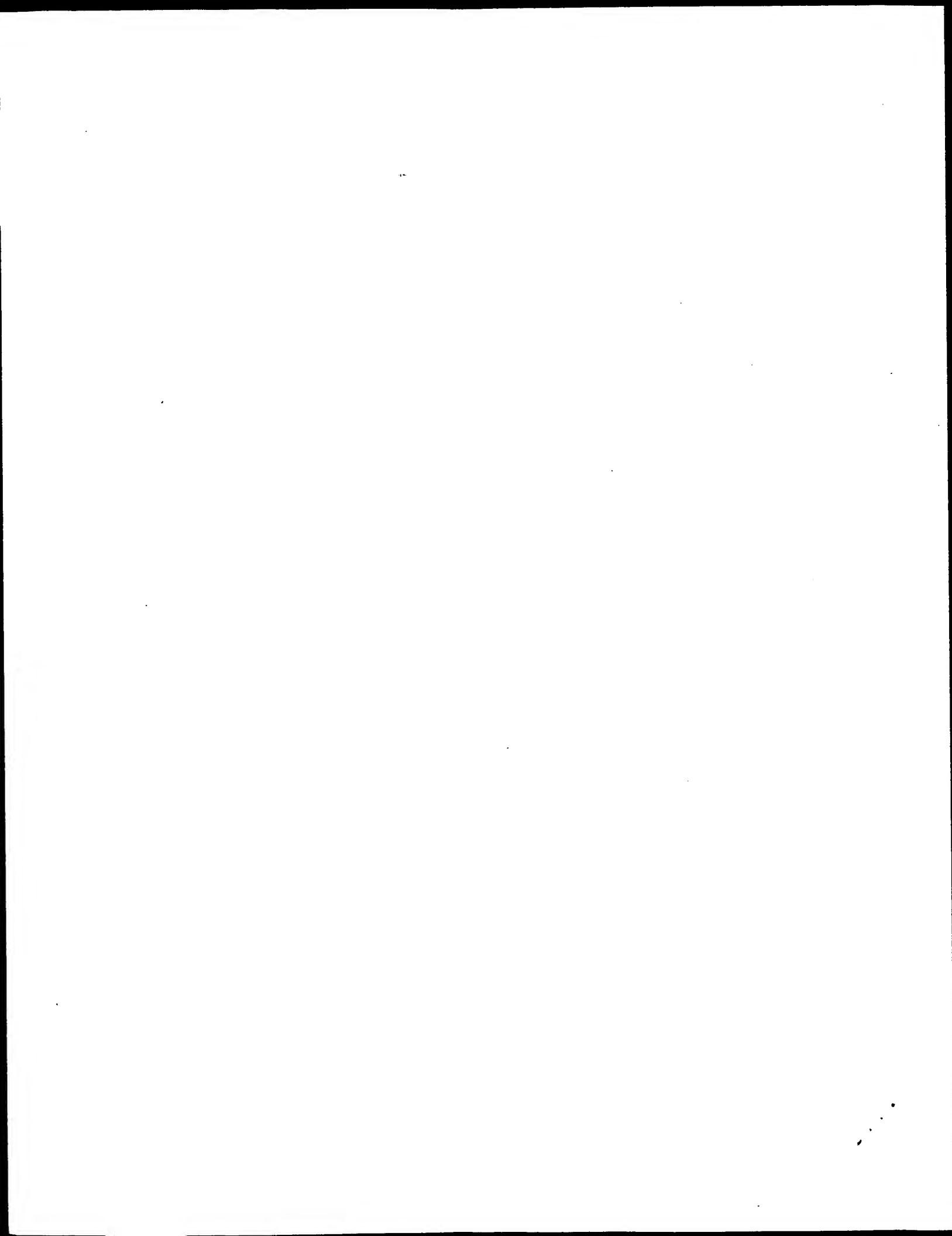
Qy 65 KC 66
Db 1544 AC 1545

Query Match 21.7%; Score 85; DB 9; Length 1593;
Best Local Similarity 30.6%; Pred. No. 1; Gaps 4;
Matches 19; Conservative 8; Mismatches 27; Indels 8; Gaps 4;

Query 12 CPSNE--IFSRCDGRCORFCPNV-VP---KPLCIKICAPGCCVRGLYLRNKKVCPRS 64
Db 1508 CPLERGFVFDCEGPPCPRTCFNQHIPLGELAAHCVRPCVPGCOCPAGLVEHEAH-CIPPE 1566

Qy 65 KC 66
Db 1567 AC 1568

Search completed: February 26, 2003, 15:10:00
Job time : 36 secs



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OM protein - protein search, using sw model

Run on: February 26, 2003, 15:04:07 ; Search time 141 Seconds
(without alignments)
306,363 Million cell updates/sec

Title: US-09-506-978-1
Perfect score: 391
Sequence: 1 GFGGLGGRGKCPNSNEIFSR CRLGYLDRNKKVCPRSKCG 67

Scoring table: BloSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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RESULT 1
US-09-506-978-1
; Sequence 1, Application US/09506978
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NANO BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/09-506,978
; CURRENT FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Apis mellifera
US-09-506-978-1

Query Match 100.0%; Score 391; DB 19;
Best Local Similarity 100.0%; Pred. No. 3.1e-2;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	391	100.0	67	19	US-09-506-978-1
2	391	100.0	67	25	US-10-174-151-3
3	391	100.0	67	25	US-09-506-978-4
4	391	100.0	69	19	US-10-204-145-1
5	391	100.0	69	25	US-10-174-151-4
6	391	100.0	69	25	US-10-204-145-2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 2
US-10-174-151-1
; Sequence 1, Application US/10174151
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/10/174,151
; CURRENT FILING DATE: 2002-06-18
; PRIORITY FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Apis mellifera
; US-10-174-151-1

Query Match 100.0%; Score 391; DB 26; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.1e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFGGLGGRKCPSENEIFSRCDGRCORFCPNVVPKPLCIKICAPGCCVRLGVLRNKKVC 60
Db 1 GGFGGLGGRKCPSENEIFSRCDGRCORFCPNVVPKPLCIKICAPGCCVRLGVLRNKKVC 60

Qy 61 VPRSKCG 67
Db 61 VPRSKCG 67

RESULT 5
US-10-174-151-2
; Sequence 2, Application US/10174151
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/10/174,151
; CURRENT FILING DATE: 2002-06-18
; PRIORITY FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Apis mellifera
; FEATURE:
; OTHER INFORMATION: Where xx at position 68 and 69 is either PL or LP.
; US-09-506-978-2

Query Match 100.0%; Score 391; DB 19; Length 69;
Best Local Similarity 100.0%; Pred. No. 3.2e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFGGLGGRKCPSENEIFSRCDGRCORFCPNVVPKPLCIKICAPGCCVRLGVLRNKKVC 60
Db 1 GGFGGLGGRKCPSENEIFSRCDGRCORFCPNVVPKPLCIKICAPGCCVRLGVLRNKKVC 60

Qy 61 VPRSKCG 67
Db 61 VPRSKCG 67

RESULT 6
US-10-204-145-2
; Sequence 2, Application US/10204145
; GENERAL INFORMATION:
; APPLICANT: Ecole Polytechnique Federale de Lausanne
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001-064 20349-543
; CURRENT APPLICATION NUMBER: US/10/204,145
; CURRENT FILING DATE: 2002-08-16
; PRIORITY APPLICATION NUMBER: U.S.S.N. 09/506,978
; PRIORITY FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Apis mellifera
; US-10-204-145-1

Query Match 100.0%; Score 391; DB 26; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.1e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFGGLGGRKCPSENEIFSRCDGRCORFCPNVVPKPLCIKICAPGCCVRLGVLRNKKVC 60
Db 1 GGFGGLGGRKCPSENEIFSRCDGRCORFCPNVVPKPLCIKICAPGCCVRLGVLRNKKVC 60

Qy 61 VPRSKCG 67
Db 61 VPRSKCG 67

RESULT 4
US-09-506-978-2
; Sequence 2, Application US/09506978
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/10/204,145
; CURRENT FILING DATE: 2002-08-16
; PRIORITY APPLICATION NUMBER: U.S.S.N. 09/506,978
; PRIORITY FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Apis mellifera
; FEATURE:
; OTHER INFORMATION: Where XX at position 68 and 69 is either PL or LP.
US-10-204-145-2

Query Match Score 100.0%; DB 26; Length 69;
Best Local Similarity 100.0%; Pred. No. 3.2e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
Qy 1 GGFGGLGGRGKCPSPNEIFSRCDGRQRCAPVNPVPLCIIKICAPGCCVRLGYLRNKKKC 60
Db 5 GGFGGLGGRGKCPSPNEIFSRCDGRQRCAPVNPVPLCIIKICAPGCCVRLGYLRNKKKC 64

Qy 61 VPRSKCG 67
Db 65 VPRSKCG 71

Qy 1 GGFGGLGGRGKCPSPNEIFSRCDGRQRCAPVNPVPLCIIKICAPGCCVRLGYLRNKKKC 60
Db 1 GGFGGLGGRGKCPSPNEIFSRCDGRQRCAPVNPVPLCIIKICAPGCCVRLGYLRNKKKC 60

Qy 61 VPRSKCG 67
Db 61 VPRSKCG 67

US-09-506-978-3
; Sequence 3, Application US/09506978
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/09/506,978
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Apis mellifera
; OTHER INFORMATION: Where XX at position 72 and 73 is either PL or LP.

Query Match Score 100.0%; DB 26; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.3e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
Qy 1 GGFGGLGGRGKCPSPNEIFSRCDGRQRCAPVNPVPLCIIKICAPGCCVRLGYLRNKKKC 60
Db 5 GGFGGLGGRGKCPSPNEIFSRCDGRQRCAPVNPVPLCIIKICAPGCCVRLGYLRNKKKC 64

Qy 61 VPRSKCG 67
Db 65 VPRSKCG 71

US-09-506-978-3
; Sequence 3, Application US/09506978
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/09/506,978
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Apis mellifera
; OTHER INFORMATION: Where XX at position 72 and 73 is either PL or LP.

Query Match Score 100.0%; DB 19; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.4e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
Qy 1 GGFGGLGGRGKCPSPNEIFSRCDGRQRCAPVNPVPLCIIKICAPGCCVRLGYLRNKKKC 60
Db 5 GGFGGLGGRGKCPSPNEIFSRCDGRQRCAPVNPVPLCIIKICAPGCCVRLGYLRNKKKC 64

Qy 61 VPRSKCG 67
Db 65 VPRSKCG 71

US-10-174-151-3
; Sequence 3, Application US/10174151
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/10/174,151
; Prior Application Number: US-09-506,978
; Prior Filing Date: 2000-02-18
; Number of Seq ID Nos: 5
; Software: PatentIn Ver. 2.0
; Seq ID No 3
; Length: 71
; Type: PRT
; Organism: Apis mellifera
; Other Information: Where XX at position 72 and 73 is either PL or LP.

Query Match Score 100.0%; DB 25; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.3e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-174-151-3
; Sequence 3, Application US/10174151
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/10/174,151
; Prior Application Number: US-09-506,978
; Prior Filing Date: 2000-02-18
; Number of Seq ID Nos: 5
; Software: PatentIn Ver. 2.0
; Seq ID No 3
; Length: 71
; Type: PRT
; Organism: Apis mellifera
; Other Information: Where XX at position 72 and 73 is either PL or LP.

Query Match Score 100.0%; DB 25; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.3e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 US-10-174-151-4
 Sequence 4 Application US/10174151
 ; GENERAL INFORMATION:
 ; APPLICANT: Spertini, Francois
 ; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
 ; FILE REFERENCE: 18519-001
 ; CURRENT APPLICATION NUMBER: US/10/174,151
 ; CURRENT FILING DATE: 2002-06-18
 ; PRIOR APPLICATION NUMBER: US/09/506,978
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 73
 ; TYPE: PRT
 ; ORGANISM: Apis mellifera
 ; FEATURE:
 ; OTHER INFORMATION: Where XX at position 72 and 73 is either PL or LP.
 ; OS-10-174-151-4

Query Match Score 391; DB 25; Length 73;
 Best Local Similarity 100.0%; Pred. No. 3.4e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFGGLGGRKCPNSNEIFSRCDGRCPNSNEIFSRCDGRCORFCPNVVPKPLCIKICAPGCVRLGYLRNKKYC 60
 Db 5 GGFGGLGGRKCPNSNEIFSRCDGRCPNSNEIFSRCDGRCORFCPNVVPKPLCIKICAPGCVRLGYLRNKKYC 64
 Qy 61 VPRSKCG 67
 Db 86 VPRSKCG 92

RESULT 14
 US-60-142-896-1491
 ; Sequence 1491 Application US/60142896
 ; GENERAL INFORMATION:
 ; APPLICANT: Keravage, Anthony
 ; TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: CLO00052
 ; CURRENT APPLICATION NUMBER: US/60/142,896
 ; CURRENT FILING DATE: 1999-07-08
 ; NUMBER OF SEQ ID NOS: 1384
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 1491
 ; LENGTH: 62
 ; TYPE: PRT
 ; ORGANISM: Drosophila
 ; OS-60-142-896-1491

Query Match Score 391; DB 27; Length 62;
 Best Local Similarity 100.0%; Pred. No. 0.0008;
 Matches 21; Conservative 8; Mismatches 26; Indels 3; Gaps 2;

Qy 11 KCPNSNEIFSRCDGRCORFCPNVVPKPLCIK-ICAPGCVRLGYLRNKKYCVRPSKC 66
 Db 4 RCPANETFLACGPBCQTCATA-TLGKPCVVRHRCPDGCYNGFARNAAGTCIPLRC 60

RESULT 15
 US-60-145-138-701
 ; Sequence 701 Application US/60145138
 ; GENERAL INFORMATION:
 ; APPLICANT: Bonazzi, Vivien
 ; TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: CLO00062
 ; CURRENT APPLICATION NUMBER: US/60/145,138
 ; CURRENT FILING DATE: 1999-07-22
 ; NUMBER OF SEQ ID NOS: 948
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 701

Query Match Score 391; DB 26; Length 73;
 Best Local Similarity 100.0%; Pred. No. 3.4e-32;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFGGLGGRKCPNSNEIFSRCDGRCPNSNEIFSRCDGRCORFCPNVVPKPLCIKICAPGCVRLGYLRNKKYC 60
 Db 5 GGFGGLGGRKCPNSNEIFSRCDGRCORFCPNVVPKPLCIKICAPGCVRLGYLRNKKYC 64
 Qy 61 VPRSKCG 67
 Db 65 VPRSKCG 71

RESULT 13
 PCT-US99-21077-2

Wed Feb 26 15:12:38 2003

us-09-506-978-1.open.rapm

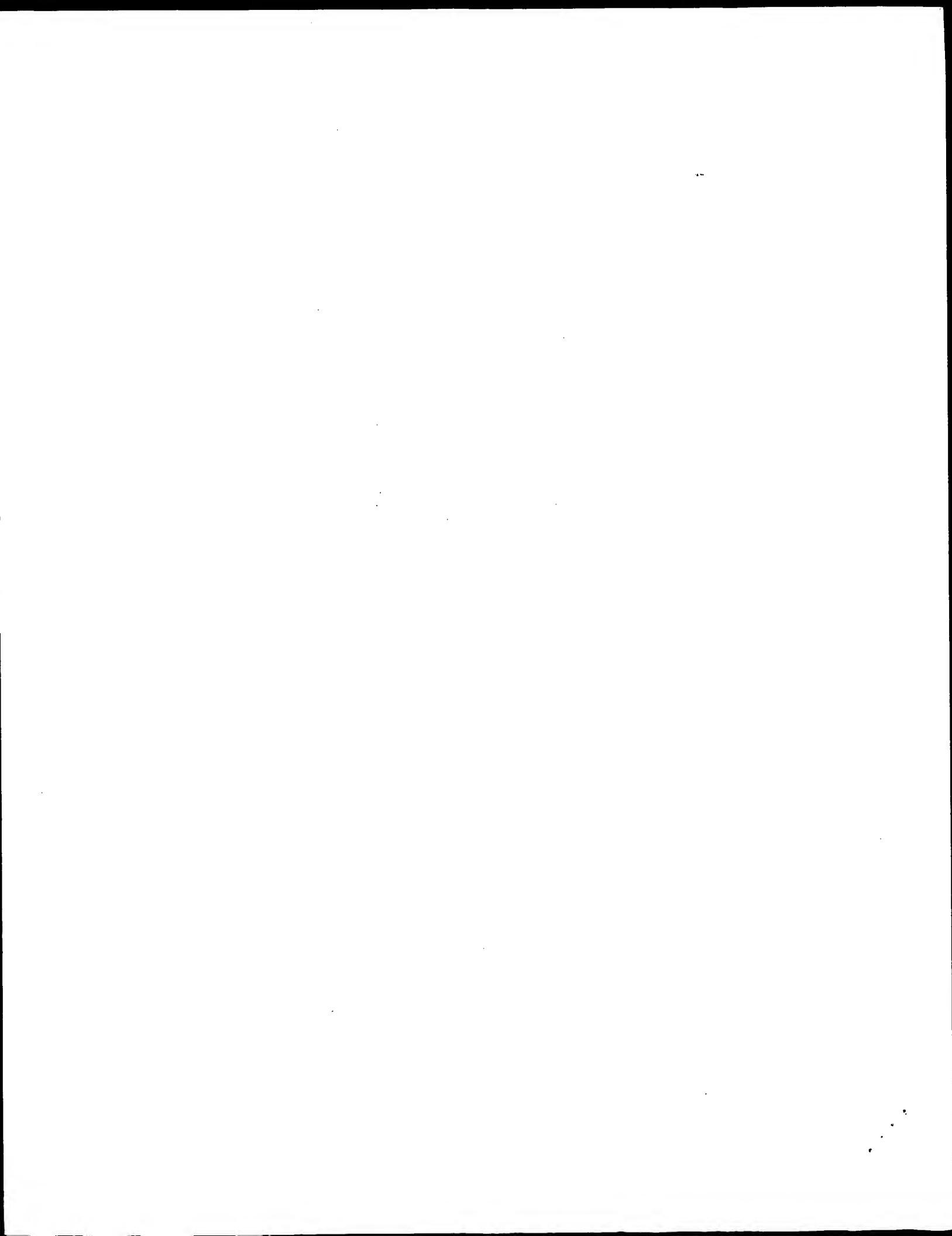
Page 5

; LENGTH: 62
; TYPE: prt
; ORGANISM: Drosophila
US-60-145-138-701

Query Match 29.0%; Score 113.5; DB 27; Length 62;
Best Local Similarity 36.2%; Pred. No. 0.0008;
Matches 21; Conservative 8; Mismatches 26; Indels 3; Gaps 2;

Qy 11 KCPSNEIFSRDGRCORFCPNVPRPLCIK -ICAPGCYCRIGYLRLNKKVCPRSKC 66
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 RCPANETFLAGPDCOTCA-TLGRCPLVHTRCPDGCICNKGPARNAAAGTCIPLRRC 60

Search completed: February 26, 2003, 15:08:48
Job time: 142 secs



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OM protein - protein search, using sw model

Run on: February 26, 2003, 15:04:32 ; Search time 23 seconds
 (without alignments)
 266.242 Million cell updates/sec

Title: US-09-506-978-1

Perfect score: 391

Sequence: 1 GGFGLGGRKCPSENIFSR.....CRUGYLRNKKRYCVPRSKCG 67

Scoring table: BL0SUM62

Gapext 0.5

Searched: 486122 seqs 91396495 residues

Total number of hits satisfying chosen parameters: 486122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 8% Maximum Match 100%

Listing first 45 summaries

Database :

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 2: /cgns_6/pctodata/2/paa/US06_NEWCOMB_pep:
 3: /cgns_6/pctodata/2/paa/US07_NEWCOMB_pep:
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 7: /cgns_6/pctodata/2/paa/US60_NEWCOMB_pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	30.4	67	6 US-10-038-854-185	Sequence 185, App
2	113	28.9	5374	6 US-10-038-248A-75	Sequence 75, Appl
3	113	28.9	5374	6 US-10-038-732-75	Sequence 75, Appl
4	113	28.9	5376	6 US-10-028-248A-74	Sequence 74, Appl
5	113	28.9	5376	6 US-10-107-783-74	Sequence 74, Appl
6	109	27.9	2601	6 US-10-028-248A-76	Sequence 76, Appl
7	109	27.9	2601	6 US-10-107-792-76	Sequence 76, Appl
8	106.5	27.2	4360	5 US-09-724-676A-66993	Sequence 66993, A
9	106.5	27.2	4360	5 US-09-724-676A-66993	Sequence 66993, A
10	98	25.1	2813	1 PCT-US02-04915-149	Sequence 149, App
11	97.5	24.9	111	1 PCT-US02-04955-379	Sequence 379, App
12	90	23.0	4219	6 US-10-085-198-2	Sequence 2, Appl
13	81	20.7	1082	6 US-10-064-237-2725	Sequence 2725, Ap
14	81	20.7	1458	1 PCT-US02-13209-25	Sequence 25, Appl
15	81	20.7	1460	1 PCT-US02-13209-24	Sequence 24, Appl
16	81	20.7	2212	6 US-10-028-248A-43	Sequence 43, Appl
17	81	20.7	2212	6 US-10-107-783-43	Sequence 43, Appl
18	81	20.7	2570	6 US-10-028-248A-42	Sequence 42, Appl
19	81	20.7	2570	6 US-10-028-782-42	Sequence 42, Appl
20	76	19.9	1568	6 US-10-265-929-17	Sequence 117, App
21	76.5	19.6	855	6 US-10-072-012-355	Sequence 355, App
22	76.5	19.6	855	6 US-10-072-012-413	Sequence 413, App
23	76.5	19.6	902	6 US-10-333-743-3	Sequence 3, Appl
24	75.5	19.3	5179	7 US-60-438-735-151	Sequence 151, App
25	73.5	18.8	855	6 US-10-072-012-356	Sequence 356, App
26	73.5	18.8	855	6 US-10-072-012-414	Sequence 414, App

ALIGNMENTS

RESULT 1 US-10-038-854-185	
GENERAL INFORMATION:	
; Sequence 185 Application US/10038854	
; GENERAL INFORMATION:	
; SPYTEK, Kimberly A	
; APPLICANT: Li, Li	
; APPLICANT: Woleinc, Adam R	
; APPLICANT: Vernet, Corinne	
; APPLICANT: Eisen, Andrew J	
; APPLICANT: Liu, Xiaohong	
; APPLICANT: Malyankar, Uriel M	
; APPLICANT: Shinkets, Richard A	
; APPLICANT: Tchernov, Velizar	
; APPLICANT: Spaderna, Steven K	
; APPLICANT: Gorman, Linda	
; APPLICANT: Kekuda, Ramesh	
; APPLICANT: Patturajan, Meera	
; APPLICANT: Gusev, Vladimir Y	
; APPLICANT: Gangolli, Esha A	
; APPLICANT: Guo, Xiaojia S	
; APPLICANT: Shenoy, Suresh G	
; APPLICANT: Rastelli, Luca	
; APPLICANT: Casman, Stacie J	
; APPLICANT: Boldog, Ferenc	
; APPLICANT: Burgess, Catherine E	
; APPLICANT: Edinger, Shlomit R	
; APPLICANT: Ellerman, Karen	
; APPLICANT: Gunther, Erik	
; APPLICANT: Smithson, Glenna	
; APPLICANT: Millet, Isabelle	
; APPLICANT: Machoudail, John R	
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same	
; FILE REFERENCE: 2140-0-230	
; CURRENT APPLICATION NUMBER: US/10/038-854	
; CURRENT FILING DATE: 2003-01-22	
; PRIOR APPLICATION NUMBER: 60/258,938	
; PRIOR FILING DATE: 2000-12-29	
; PRIOR APPLICATION NUMBER: 60/259,415	
; PRIOR FILING DATE: 2001-01-02	
; PRIOR APPLICATION NUMBER: 60/259,785	
; PRIOR FILING DATE: 2001-01-04	
; PRIOR APPLICATION NUMBER: 60/269,814	
; PRIOR FILING DATE: 2001-02-20	
; PRIOR APPLICATION NUMBER: 60/279,832	
; PRIOR FILING DATE: 2001-03-29	
; PRIOR APPLICATION NUMBER: 60/279,833	
; PRIOR FILING DATE: 2001-03-29	
; PRIOR APPLICATION NUMBER: 60/279,863	
; PRIOR FILING DATE: 2001-03-29	

PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 185
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-248A-185

Query Match 28.9%; Score 113; DB 6; Length 5374;
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 75
; LENGTH: 5374
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-038-248A-75

Query Match 28.9%; Score 113; DB 6; Length 5374;
; Best Local Similarity 37.5%; Pred. No. 0.0014;
; Matches 24; Conservative 8; Mismatches 22; Indels 10; Gaps 3;

Query Match 28.9%; Score 113; DB 6; Length 5374;
; Best Local Similarity 37.5%; Pred. No. 0.0014;
; Matches 24; Conservative 8; Mismatches 22; Indels 10; Gaps 3;

QY 11 KCPSENIFSRCDGRQRFNPKVPC-----IKICAPGCVCRLGYLRLGKVKVCPR 63
Db 4741 KCPANSILTHCLPCTCPSCSN - PDGRCEGTSHKAPSTCRGSCVCPGYLLN-KDTCVHK 4797

Query Match 30.4%; Score 119; DB 6; Length 67;
; Best Local Similarity 37.3%; Pred. No. 1.3e-05;
; Matches 25; Conservative 7; Mismatches 23; Indels 12; Gaps 3;

QY 64 SKCG 67
Db 4798 NQCG 4801

RESULT 3
US-10-107-782-75

Sequence 75, Application US/10107782

GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangoli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malvankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shinkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glenna,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Tapier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222C1P
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 10/028,248
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262,959
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272,408
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/245,189
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308,039
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311,266
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/279,344
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CuraseqList version 0.1
SEQ ID NO: 75
LENGTH: 5374

Query Match 30.4%; Score 119; DB 6; Length 67;
; Best Local Similarity 37.3%; Pred. No. 1.3e-05;
; Matches 25; Conservative 7; Mismatches 23; Indels 12; Gaps 3;

QY 64 SKCG 67
Db 4798 NQCG 4801

RESULT 2
US-10-028-248A-75

Sequence 75, Application US/10028248A

GENERAL INFORMATION:
; APPLICANT: Shimkess, Richard
; APPLICANT: Patterson, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoj, Suresh
; APPLICANT: Spytak, Kimberly
; APPLICANT: Gangoli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glenna
; APPLICANT: Sciore, Paul
; APPLICANT: Tapier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: 21402-222C1P
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 10/028,248
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262,959
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272,408
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/245,189
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308,039
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311,266
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/279,344
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CuraseqList version 0.1
SEQ ID NO: 75
LENGTH: 5374

;

TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-782-75

Query Match 28.9%; Score 113; DB 6; Length 5374;
Best Local Similarity 37.5%; Pred. No. 0.0014;
Matches 24; Conservative 8; Mismatches 22; Indels 10; Gaps 3;

Qy 11 KCP\$NEIFSRCDGRCQRFCPNVVKPLC-----IKICAPGVCRIGYLRNKKVVCVPR 63
Db 4743 KCPANSLYTHCLPCLPSCSN - PDGRCEGTSHKAPSTCREGCVCQPGYLN-KDTCVHK 4799

Qy 64 SKCG 67
Db 4800 NQCG 4803

RESULT 5
US-10-107-782-74
Sequence 74, Application US/10107782
GENERAL INFORMATION:
; Sequence 74, Application US/10028248A
; GENERAL INFORMATION:
; APPLICANT: Shimbets, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Maljankar, Uriel
; APPLICANT: Sheony, Suresh
; APPLICANT: Spyek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Bolidog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glenda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: 21402-222CIP
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 10/028-248
PRIOR FILING DATE: 2004-12-19
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262,959
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272,408
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285,189
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308,039
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311,266
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/279,344
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 74
LENGTH: 5376
TYPE: PRT
ORGANISM: Homo sapiens
US-10-107-782-74

Query Match 28.9%; Score 113; DB 6; Length 5376;
Best Local Similarity 37.5%; Pred. No. 0.0014;
Matches 24; Conservative 8; Mismatches 22; Indels 10; Gaps 3;

Qy 11 KCP\$NEIFSRCDGRCQRFCPNVVKPLC-----IKICAPGVCRIGYLRNKKVVCVPR 63
Db 4743 KCPANSLYTHCLPCLPSCSN - PDGRCEGTSHKAPSTCREGCVCQPGYLN-KDTCVHK 4799

Qy 64 SKCG 67 :|||
 Db 4800 NQCG 4803

RESULT 6
 US-10-028-248A-76
 ; Sequence 76, Application US/10028248A

; GENERAL INFORMATION:
 ; APPLICANT: Shimkets, Richard
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Cashman, Stacie
 ; APPLICANT: Malvankar, Uriel
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Gangolli, Esha
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: Taupier, Raymond J
 ; APPLICANT: Smithson, Glenna
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Colman, Steven
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Si, Jingsheng
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Stone, David
 ; APPLICANT: Sciore, Paul
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Rothenberg, Mark
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides and Methods of Use
 ; TITLE OF INVENTION: Thereof
 ; FILE REFERENCE: 21402-222CIP
 ; CURRENT APPLICATION NUMBER: US/10/028,248A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/256619
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: 60/262959
 ; PRIOR FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: 60/272408
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 60/285189
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/308039
 ; PRIOR FILING DATE: 2001-07-26
 ; PRIOR APPLICATION NUMBER: 60/311266
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 60/279,344
 ; PRIOR FILING DATE: 2001-03-28
 ; NUMBER OF SEQ ID NOS: 215
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 76
 ; LENGTH: 2601
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-028-248A-76

Query Match 27.9%; Score 109; DB 6; Length 2601;
 Best Local Similarity 35.3%; Pred. No. 0.0021; Mismatches 11; Indels 20; Gaps 4;

Qy 11 KCPSENEIFSRQ-----DGRCQRFCPNNVVKPLCIKICARGCVYRLGVLRNKKKV 59
 Db 2210 ECPAYSSYTNCPLSPSCWDLGRCE---GAKVP----SACAEGCICQPGYVLSEDK- 2260

Qy 60 CYPRSKCG 67
 Db 2261 CYPRSQCG 2268

RESULT 8
 US-09-724-676-66993
 ; Sequence 66993, Application US/09724676
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD

PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,605
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; REMAINING PRIOR APPLICATION DATA REMOVED - SEE FILE WRAPPER OR PAIM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 4219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-2

Query Match 23.0%; Score 90; DB 6; Length 4219;
Best Local Similarity 40.3%; Pred. No. 0.3%; Indels 8; Gaps 5;
Matches 27; Conservative 5; Mismatches 27; Indels 8; Gaps 5;

Qy 4 GLGGRGK--CPSNEIFSRCDGRCQRCPNVPKPLCIKICAPGCCYVRLGYLRNKKK 59
Db 2988 GPGWRSRSRRLCPSPG-DSSCPGDATOEFP-CSPIPICTGFCAPICTGPGLFLHNRAS-- 3043

Qy 60 CVPRSKC 66
Db 3044 CLPRSRKC 3050

RESULT 13
US-10-264-237-2725
; Sequence 2725, Application US/10264237
GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 2725
; LENGTH: 1082
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2725

Query Match 20.7%; Score 81; DB 6; Length 1082;
Best Local Similarity 31.3%; Pred. No. 1%; Indels 18; Gaps 4;
Matches 23; Conservative 9; Mismatches 22; Indels 18; Gaps 4;

Qy 5 GLGGRGKPSNEIFSRCDGRCQRCPNVPKPLCIKICAPGCCYVRLGYLR 54
Db 544 GLGGSGSCFCDEGWTGPCEVQEL--QPVCTPPCAPEAVRAGNSCECSLGY-E 595

Qy 55 NKKKVCVPRSKC 66
Db 596 GDGRVCTVADLC 607

RESULT 14
PCT-US02-13209-25
; Sequence 25, Application PC/TUS0213209
GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL H.
; TITLE OF INVENTION: METHODS OF USING A HYALURONAN RECEPTOR
; FILE REFERENCE: 619758-8/JP/286,468
; CURRENT APPLICATION NUMBER: PCT/US02/13209
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,468
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 09/842,930
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 24
; LENGTH: 1460
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13209-24

Query Match 20.7%; Score 81; DB 1; Length 1460;
Best Local Similarity 31.3%; Pred. No. 1.3%; Indels 18; Gaps 4;
Matches 23; Conservative 9; Mismatches 22; Indels 18; Gaps 4;

Qy 5 GLGGRGKPSNEIFSRCDGRCQRCPNVPKPLCIKICAPGCCYVRLGYLR 54
Db 922 GLGGSGSCFCDEGWTGPCEVQEL--QPVCTPPCAPEAVRAGNSCECSLGY-E 973

Qy 55 NKKKVCVRSKC 66
Db 974 GDGRVCTVADLC 985

Search completed: February 26, 2003, 15:09:19
Job time : 25 secs

RESULT 14
PCT-US02-13209-25
; Sequence 25, Application PC/TUS0213209
GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL H.
; TITLE OF INVENTION: METHODS OF USING A HYALURONAN RECEPTOR
; FILE REFERENCE: 619758-8/JP/286,468
; CURRENT APPLICATION NUMBER: PCT/US02/13209

Result No.	Score	Query	Match	Description
		No.	Length	DB ID
1	391	100.0	92	4 US-09-394-630-2
2	107.5	27.5	2476	2 US-09-394-630-2
3	106.5	27.2	2594	4 US-09-394-630-2
4	106.5	27.2	5405	4 US-09-394-630-2
5	100	25.6	84	2 US-09-394-630-2
6	100	25.6	84	2 US-09-394-630-2
7	100	25.6	84	2 US-09-394-630-2
8	100	25.6	84	2 US-09-394-630-2
9	100	25.6	84	2 US-09-394-630-2
10	100	25.6	84	3 US-09-394-630-2
11	100	25.6	84	3 US-09-394-630-2
12	100	25.6	84	3 US-09-394-630-2
13	100	25.6	84	3 US-09-394-630-2
14	100	25.6	84	3 US-09-394-630-2
15	100	25.6	84	3 US-09-394-630-2
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24	100	25.6	91	3 US-09-394-630-2
25	100	25.6	91	3 US-09-394-630-2
26	100	25.6	91	3 US-09-394-630-2
27	100	25.6	91	3 US-09-394-630-2
28	100	25.6	91	3 US-09-394-630-2
29	98	25.1	91	3 US-09-394-630-2
30	91	23.3	82	2 US-09-394-630-2
31	91	23.3	82	2 US-09-394-630-2
32	91	23.3	82	2 US-09-394-630-2
33	91	23.3	82	2 US-09-394-630-2
34	91	23.3	82	2 US-09-394-630-2
35	91	23.3	82	2 US-09-394-630-2
36	91	23.3	82	2 US-09-394-630-2
37	91	23.3	82	2 US-09-394-630-2
38	91	23.3	82	2 US-09-394-630-2
39	91	23.3	82	2 US-09-394-630-2
40	91	23.3	82	2 US-09-394-630-2
41	91	23.3	82	2 US-09-394-630-2
42	91	23.3	82	2 US-09-394-630-2
43	91	23.3	82	3 US-09-394-630-2
44	91	23.3	82	3 US-09-394-630-2
45	91	23.3	82	3 US-09-394-630-2

STATE: Texas
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/276,967
 FILING DATE: Submitted Herewith
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: UTSD:418\KIT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713-787-1400
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2416 amino acids
 TYPE: amino acid
 STRANDBNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: protein
 S-08-276-967-2

Query Match 27.5%; Score 107.5; DB 2; Length 2476;
 Best Local Similarity 33.3%; Pred. No. 0.0038;
 Matches 22; Conservative 9; Mismatches 18; Indels 17; Gaps 3;

Y 11 KCPNSNEIFSRDGRC-----QRFCPNVVKPLKIKACAGCVCRLGYLRNKKVCV 61
 b 1455 KCPGSSSTCTANCPATCLSNNPSYCFSTLP-----CAEGCECORGHILSGTS-CV 1506

Query Match 27.5%; Score 107.5; DB 2; Length 2476;
 Best Local Similarity 33.3%; Pred. No. 0.0038;
 Matches 22; Conservative 9; Mismatches 18; Indels 17; Gaps 3;

Y 62 PRSGCG 67
 b 1507 PLSOGC 1512

RESULT 3
 Sequence 7, Application US/08718388
 Patent No. 6271362

GENERAL INFORMATION:
 APPLICANT: MORIKAWA, MINORU
 APPLICANT: HARADA, NAOKI
 TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 29

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/718,388
 FILING DATE: 08/08/1998

CLASsIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 0230-111
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5405 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 S-08-718-388-9

RESULT 4
 Sequence 9, Application US/08718388
 Patent No. 6271362

GENERAL INFORMATION:
 APPLICANT: MORIKAWA, MINORU
 APPLICANT: HARADA, NAOKI
 TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/718,388
 FILING DATE: 08/08/1998

CLASsIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 0230-111
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5405 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 S-08-718-388-9

RESULT 5
 Sequence 5, Application US/08465380
 Patent No. 5863894

GENERAL INFORMATION:
 APPLICANT: MORIKAWA, MINORU
 APPLICANT: HARADA, NAOKI
 TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/718,388
 FILING DATE: 08/08/1998

CLASsIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 0230-111
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5405 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 S-08-718-388-9

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,
Joris H.L. Mensens, Marc J. Lauwersys,

APPLICANT: Yves R. Laroché, Laurent S. Jespers,
Yannick G.J. Gansmans, Matthew Moyle,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOAGULANT

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C., DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486-397

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/486-397

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 213/269

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Anacyclostoma caninum

US-08-486-380-59

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Anacyclostoma caninum

US-08-486-397-59

Query Match 25.6%; Score 100; DB 2; Length 84;

Best Local Similarity 30.4%; Pred. No. 0.00097;

Matches 21; Conservative 8; Mismatches 24; Indels 16; Gaps 3;

Db 62 DKCVSAEDC 70

RESULT 7 US-08-486-397-59

Sequence 59, Application US/08486397

Patent No. 5866542

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,
Joris H.L. Mensens, Marc J. Lauwersys,

APPLICANT: Yves R. Laroché, Laurent S. Jespers,
Yannick G.J. Gansmans, Matthew Moyle,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOAGULANT

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

ZIP: 90071 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 OPERATING SYSTEM: IBM P.C., DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,399
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY / AGENT INFORMATION:
 NAME: FIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 213-1/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEXFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 84 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Anacyclostoma caninum
 -08-486-399-29

Query Match 29
 Best Local Similarity 21; Matches 21; Conservative 8; Mismatch 11
 11 KCPSBEIFSRDGRCQRFC-----PNN
 11 | | : | : | : | : | : | : |
 5 QCGBEKKYDSCGSKECDKCKYDGVWEEDDEEPNV

58	KVCYPRSKC	66
62	DRKCVSAEDC	70

-08-461-965-59
 Sequence 59, Application US/08461965
 Patent No. 5,572,098
 GENERAL INFORMATION:
 APPLICANT: George P. Vlasuk, Patrice H. Joris H. L. Mensens, Marc J. Yves R. Laroche, Laurent S.
 APPLICANT: Yannick G.J. Ganssmans, Mathieu Peter W. Bergman
 APPLICANT: Peter W.
 TITLE OF INVENTION: NEMATOIDE - EXTRACTED TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C., DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:

FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 219/7136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
FORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
DIOLECULE TYPE: peptide
POLYMER SOURCE: linear
ORGANISM: Ancylostoma caninum
MATERIAL SOURCE: 614-611-59

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Query Match      25.68;  Score 100;  DB 2;  Length 84;
Best Local Similarity 30.48;  Pred. NO. 0.00097;
Matches 21;  Conservative 8;  Mismatches 24;  Indels 16

11 KCP$NEF$SRC$DOR-CQDFC-----:PNVVKPLC1K1CAPGCVCRGYL
  :| 1| :| 1| :| 1| :| 1| :| 1| :| 1| :| 1| :| 1| :| 1| :| 1| :
  5 QCGENEKYDSCS$KECDKCKYDGVEEDEENVN--PCLVRYCHQDCVCEBGFYI

58 KVCVP$RKC 66
  ||| |
  62 DVCVACATC 70

```

RESULT 10
5-09-249-471-59
Sequence 59. Application #S/09249471

Patent No. 6010441
GENERAL INFORMATION:
APPLICANT: Vlasiuk, George Phillip
APPLICANT: Staessens, Patrick Eric Hugo
APPLICANT: Mervans, Joris Hilda Lieven
APPLICANT: Lawereys, Marc Josef
APPLICANT: Larache, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Ganssema, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergman, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/1323
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 3,0,158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: *Ancyclostoma caninum*
US-09-249-471-59

Query Match 25.6%; Score 100; DB 3; Length 84;
 Best Local Similarity 30.4%; Pred. No. 0.00097;
 Matches 21; Conservative 8; Mismatches 24; Indels 16; Gaps 3;

Qy	11	KCPNSNEIFSRCDR-CQRPC-----	-PNVVPKPLCIKICAPGEVCRUGYLRNKK 57
Db	5	QCGENEKYDGSCKSKEDCKKYDGVEEEDEDPNV--	-PCLVRVCHQDPCVCEEGFYRNKD 61
Qy	58	KVCVPRSKC 66	
Db	62	DKCVSAEDC 70	

RESULT 11
 US-09-249-472-59 Application US/09249472
 GENERAL INFORMATION:
 Patent No. 6046318
 Sequence 59, Application US/09249472
 APPLICANT: Vlaasuk, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwereys, Marc Josef
 APPLICANT: Larocque, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Ganssmans, Yannick Georges Jozef
 APPLICANT: Moyle, Matthew W.
 BERGUM, Peter W.
 TITLE OF INVENTION: NEMATO-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700

STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/249,472
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/809,455
 FILING DATE: April 17, 1997
 APPLICATION NUMBER: PCT/US95/13231
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 216/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: 67-3510
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 84 amino acids
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE: Anicylostoma caninum
 US-09-249-472-59

Query Match 25.6%; Score 100; DB 3; Length 84;
 Best Local Similarity 30.4%; Pred. No. 0.00097;
 Matches 21; Conservative 8; Mismatches 24; Indels 16; Gaps 3;

Qy 11 KCPSENIFSRCDGR-CORFC-----PNNVPKPLCIKICAPGCCVRLGYLRRNKK 57
 Db 5 QCGENEKYDSCGSKECDRKYDVEEEDDEPNV--pCLVRVCHODCVCEEGFTRNKD 61

Query Match 25.6%; Score 100; DB 3; Length 84;
 Best Local Similarity 30.4%; Pred. No. 0.00097;
 Matches 21; Conservative 8; Mismatches 24; Indels 16; Gaps 3;

Qy 58 KVCVPRSKC 66
 Db 62 DKCVSAEDC 70

RESULT 12
 US-09-249-451-59
 Sequence 59, Application US/09249451
 Patent No. 6087487
 GENERAL INFORMATION:
 APPLICANT: Vlasuk, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwerys, Marc Josef
 APPLICANT: Laroche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gansmans, Yannick Georges Jozef
 APPLICANT: Moyle, Matthew
 APPLICANT: Belgium, Peter W.
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
 ; TITLE OF INVENTION: PROTIN
 ; NUMBER OF SEQUENCES: 356
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/249,451
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/809,455
 ; FILING DATE: April 17, 1997
 ; APPLICATION NUMBER: pcy/US95/13231
 ; FILING DATE: October 17, 1995
 ; APPLICATION NUMBER: 08/486,399
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/465,380
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/461,965
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/326,110
 ; FILING DATE: October 18, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BIGGS, SUZANNE L.
 ; REGISTRATION NUMBER: 30,158
 ; REFERENCE/DOCKET NUMBER: 216/270
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 59:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 84 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Anicylostoma caninum
 ; US-09-249-451-59

Query Match 25.6%; Score 100; DB 3; Length 84;
 Best Local Similarity 30.4%; Pred. No. 0.00097;
 Matches 21; Conservative 8; Mismatches 24; Indels 16; Gaps 3;

Qy 11 KCPSENIFSRCDGR-CORFC-----PNNVPKPLCIKICAPGCCVRLGYLRRNKK 57
 Db 5 QCGENEKYDSCGSKECDRKYDVEEEDDEPNV--pCLVRVCHODCVCEEGFTRNKD 61

Query Match 25.6%; Score 100; DB 3; Length 84;
 Best Local Similarity 30.4%; Pred. No. 0.00097;
 Matches 21; Conservative 8; Mismatches 24; Indels 16; Gaps 3;

Qy 58 KVCVPRSKC 66
 Db 62 DKCVSAEDC 70

RESULT 13
 US-08-809-455-59
 Sequence 59, Application US/08809455
 Patent No. 6080916
 GENERAL INFORMATION:
 APPLICANT: Vlasuk, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwerys, Marc Josef
 APPLICANT: Laroche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gansmans, Yannick Georges Jozef
 APPLICANT: Moyle, Matthew
 APPLICANT: Belgium, Peter W.
 APPLICANT: Stanssens, Patrick Eric Hugo

Query Match	25.6%	Score 100;	DB 3;	Length 84;
Best Local Similarity	30.4%	Pred. No.	0.00007;	
Matches	21;	Conservative	8;	Mismatches 24;
				Indels
Qy	11	KCPSNEIFSRCDGR-CORFC-----	PNVYPKPLCIKTCAPGCVCRIG	
	:	: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : :	
Dbx	5	QCGENEKYDSCGSKEDKCKYDGVVEEDDEPNNV--	PCLIVRWHODCVCEEE	

Db 5 QCGENEKYDSGSKEDKCKYDGVEEDDEEPNV--PCLVRVCHQDCVC3EGFYRND 61
 Qy 58 KVCYPRSKC 66
 Db 62 DKCVSAEDC 70

RESULT 15
 Sequence 59, Application US/09249448
 Patent No. 6121435

GENERAL INFORMATION:
 APPLICANT: Vlasek, George Phillip
 APPLICANT: Stassens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauverey, Marc Josef
 APPLICANT: Larche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Ganssemans, Yannick Georges Jozef
 APPLICANT: Moyse, Matthew
 APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 TITLE OF INVENTION: INHIBITORS AND ANTI COAGULANT
 NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C., DOS 5.0
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/249,448
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/809,455
 FILING DATE: April 17, 1997
 APPLICATION NUMBER: PCP70595/13231
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

SEQUENCE CHARACTERISTICS:
 LENGTH: 84 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Ancyclostoma caninum

RESULT 3
S35098 trypsin inhibitor - pig roundworm
C;Species: Ascaris suum (pig roundworm)
C;Date: 19 Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S35098
R;Grönblom, A.M.; Nilges, M.; Peanashy, R.J.; Clore, G.M.
Biochemistry 29, 183-189, 1990
A;Title: Sequential resonance assignment and secondary structure determination of the Ascaris suum trypsin inhibitor
A;Reference number: S35098; MUID:90212567; PMID:2322539
A;Accession: S35098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-62 <KID>
C;Superfamily: roundworm trypsin inhibitor

Query Match	18.0%	Score 70.5;	DB 2;	Length 62;
Best Local Similarity	29.3%	Pred. No. 2.1;		
Matches 18;	Conservative	12;	Indels 9;	Gaps 5;
Qy	11	KCPS-NEIFSRCDGRQRFC-PNVPKPLIKICAP--GCVCRLGYLNKKVCPVSK 65		
Db	4	KCTKPNEQWTRCGG-CEGTCAQKIVP--CTRECKPPRCECIASAGFVRDAQNCIKFED 59		
Qy	66	C 66		
Db	60	C 60		

RESULT 4
S31723 metallothionein - northern pike
C;Species: Esox lucius (northern pike)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
C;Accession: S38334; S17175; S15503; S31723
R;Kille, P.; Kay, J.; Sweeney, G.E.
Biochim. Biophys. Acta 1216, 55-64, 1993
A;Title: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant fish
A;Reference number: S38334; MUID:94032483; PMID:8218416
A;Accession: S38334
A;Molecule type: DNA
A;Residues: 1-60 <KID>
A;Cross-references: EMBL:X70042; NID:g62782; PIDN:CAA49636_1; PID:g62783
A;Note: the authors translated the codon ACT for residue 9 as Ser
R;Kille, P.; Stephens, P.E.; Kay, J.
Biochim. Biophys. Acta 1089, 407-410, 1991
A;Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone loach and lamprey
A;Reference number: S16996; MUID:91316146; PMID:1859844
A;Accession: S17175
A;Molecule type: mRNA
A;Residues: 1-60 <KID>
A;Cross-references: EMBL:X59392; NID:g62780; PIDN:CAA42035_1; PID:g62781
C;Genetics:

Query Match	17.6%	Score 69;	DB 2;	Length 60;	
Best Local Similarity	37.0%	Pred. No. 2.9;			
Matches 19;	Conservative	3;	Mismatches 18;	Indels 14;	Gaps 3;
Qy	7	GGRKCPSEIIFSRCDGRQRFCPNVPKPLIKICAPGCCYCRIGYLRLNKKV 60			
Db	15	GGSCKC-SNCACTSCKKSCCPGSDCSK-----CASGCVG-----KGKTC 54			

RESULT 5
B27490 metallothionein B - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 18-Jul-1988 #sequence_revision 18-Jul-1988 #text_change 20-Aug-1999

C;Accession: A30818; B27490; S16997; S15509
 R;Zafarullah, M.; Bonham, K.; Gedamu, L.
 N;Cell. Biol. 8, 449-447, 1988
 A;Title: Structure of the rainbow trout metallothionein B gene and characterization of the metallothionein B gene and characterization o
 C;Accession number: A30818; MUID:318557
 A;Molecule type: DNA
 A;Residues: 1-60 <ZAF>
 A;Cross-references: GB:MI18104; NID:g213816; PIDN:AAA49566_1; PID:g213817
 R;Bonham, K.; Zafarullah, M.; Gedamu, L.
 DNA 6, 519-528, 1987
 A;Title: The rainbow trout metallothioneins: molecular cloning and characterization o
 A;Reference number: A27490; MUID:88111026; PMID:2448099
 A;Accession: B27490
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-60 <BON>
 A;Cross-references: GB:MI18104; NID:g213816; PIDN:AAA49566_1; PID:g213817
 R;Kille, P.; Stephens, P.E.; Kay, J.
 Biochim. Biophys. Acta 1089, 407-410, 1991
 A;Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone loach and lamprey
 A;Reference number: S16996; MUID:91316146; PMID:1859844
 A;Accession: S16997
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-60 <SKIL>
 A;Cross-references: EMBL:X59394; NID:g64332; PIDN:CAA42037_1; PID:g64333
 C;Superfamily: metallothionein

Query Match	17.6%	Score 69;	DB 2;	Length 60;	
Best Local Similarity	37.0%	Pred. No. 2.9;			
Matches 20;	Conservative	2;	Mismatches 18;	Indels 14;	Gaps 3;
Qy	7	GGRKCPSEIIFSRCDGRQRFCPNVPKPLIKICAPGCCYCRIGYLRLNKKV 60			
Db	15	GGSCKC-SNCACTSCKKSCCPGSDCSK-----CASGCVG-----KGKTC 54			

RESULT 6
S30367 metallothionein - plaice
C;Species: Pleuronectes platessa (plaice)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C;Accession: S30567
R;Leaver, M.J.; George, S.G.
Submitted to the EMBL Data Library, November 1990
A;Reference number: S30567
A;Accession: S30567
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-60 <LEA>
A;Cross-references: EMBL:X56743; NID:g64237; PIDN:CAA40067_1; PID:g64238
C;Superfamily: metallothionein

Query Match	17.4%	Score 68;	DB 2;	Length 60;	
Best Local Similarity	35.2%	Pred. No. 3.7;			
Matches 19;	Conservative	3;	Mismatches 18;	Indels 14;	Gaps 3;
Qy	7	GGRKCPSEIIFSRCDGRQRFCPNVPKPLIKICAPGCCYCRIGYLRLNKKV 60			
Db	15	GGSCTC-KNCSCITCNCSCCPGSDCSK-----CASGCVG-----KGKTC 54			

RESULT 7
A53640 metallothionein 4 - human
N;Alternate names: metallothionein IV
C;Species: Homo sapiens (man)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 03-Dec-1999
C;Accession: A53640
R;Quaife, C.J.; Findley, S.D.; Erickson, J.C.; Froelick, G.J.; Kelly, E.J.; Zambrowicz, B.; Biochemistry 33, 7260-7259, 1994
A;Title: Induction of a new metallothionein isoform (MT-IV) occurs during differentiation

A; Reference number: A53640; MUID:94271779; PMID:8003488
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-62 <QDA>
A; Cross-references: GB:U07807; NID:9465264; PIDN:AAA20232.1.; PMID:g516535
C; Genetics:
A; Introns: 11/1; 33/1
C; Superfamily: metallothionein

Query Match 17.1%; Score 67; DB 2; Length 62;
Best Local Similarity 35.1%; Pred. No. 4.7;
Matches 20; Conservative 8; Mismatches 23; Indels 6; Gaps 4;

Qy 7 GGRGKCPNSEIFSRCDGR-CORFCPNVVKPLC1K1KAPGCYCRGLYLNKKVCP 62
Db 11 GGICMGDNCKCTTCNCRKSCCPCCP-PGCAK-CARICKGG---SDKCSCCP 62

RESULT 8
B53640 metallothionein IV - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
C;Accession: B53640
R;Quaife, C.J.; Findley, S.D.; Erickson, J.C.; Froelick, G.J.; Kelly, E.J.; Zambrowicz, Biochemistry 33, 7250-7259, 1994
A;Title: Induction of a new metallothionein isoform (MT-IV) occurs during differentiation
A;Reference number: A53640; MUID:94271779; PMID:8003488
A;Accession: B53640
A;Status: preliminary
A; Molecule type: DNA
A; Residues: 1-62 <QDA>
A; Cross-references: GB:U07808; NID:9466266; PIDN:AAA20233.1.; PMID:g516536
C; Genetics:
A; Introns: 11/1; 33/1
C; Superfamily: metallothionein

Query Match 16.6%; Score 65; DB 2; Length 62;
Best Local Similarity 33.9%; Pred. No. 7.4;
Matches 21; Conservative 4; Mismatches 27; Indels 10; Gaps 4;

Qy 1 GGFGLGGRKCPNSEIFSRCDGR-CORFCPNVVKPLC1K1KAPGCYCRGLYLNKKV 60
Db 11 GGICMGDNCKCTTCNCRKSCCPCCP-KTCRKSCCP-CARGC1GG---SDKCSC 60

Qy 61 VP 62
Db 61 CP 62

RESULT 9
A37425 metallothionein 2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A37425
R;Wagner, G.; Neuhaus, D.; Neuhauer, E.; Vasaek, M.; Kaegi, J.H.R.; Wuehrich, K., Eur. J. Biochem. 157, 275-289, 1986
A;Title: Sequence-specific (¹H)-NMR assignments in rabbit-liver metallothionein-2.
A;Reference number: A37425; MUID:86220204; PMID:3709538
A;Accession: A37425
A;Status: preliminary
A; Molecule type: Protein
A; Residues: 1-61 <PAG>
C; Superfamily: metallothionein

Query Match 15.9%; Score 62; DB 2; Length 61;
Best Local Similarity 38.5%; Pred. No. 14;
Matches 15; Conservative 2; Mismatches 10; Indels 12; Gaps 3;

Qy 11 KCPNSEIFSRCDGR-CORFCPNVVKPLC1K1KAPGCYCR 49

RESULT 10
S54335 metallothionein-2c - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S54335
R;Hunziker, P.E.; Kaur, P.; Wan, M.; Kaenzig, A., Biochem. J. 306, 265-270, 1995
A;Title: Primary structures of seven metallothioneins from rabbit tissue.
A;Reference number: S54331; MUID:95169065; PMID:7864820
A;Accession: S54335
A;Status: preliminary
A; Molecule type: protein
A; Residues: 1-62 <HUN>
C; Superfamily: metallothionein

Query Match 15.9%; Score 62; DB 2; Length 62;
Best Local Similarity 38.5%; Pred. No. 15;
Matches 15; Conservative 2; Mismatches 10; Indels 12; Gaps 3;

Qy 11 KCPNSEIFSRCDGR-CORFCPNVVKPLC1K1KAPGCYCR 49
Db 26 KCTS- --- -CKRSCSCCP---PGCAK-CAQGICK 52

RESULT 11
S54336 metallothionein-2a - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S54336
R;Hunziker, P.E.; Kaur, P.; Wan, M.; Kaenzig, A., Biochem. J. 306, 265-270, 1995
A;Title: Primary structures of seven metallothioneins from rabbit tissue.
A;Reference number: S54331; MUID:95169065; PMID:7864820
A;Accession: S54336
A;Status: preliminary
A; Molecule type: protein
A; Residues: 1-62 <HUN>
C; Superfamily: metallothionein

Query Match 15.9%; Score 62; DB 2; Length 62;
Best Local Similarity 38.5%; Pred. No. 15;
Matches 15; Conservative 2; Mismatches 10; Indels 12; Gaps 3;

Qy 11 KCPNSEIFSRCDGR-CORFCPNVVKPLC1K1KAPGCYCR 49
Db 26 KCTS- --- -CKRSCSCCP---PGCAK-CAQGICK 52

RESULT 12
A23889 metallothionein 1 - bovine (tentative sequence)
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 28-Apr-1995.
C;Accession: A23889
R;Nunger, K.; Germann, U.; Beltramini, M.; Niedermann, D.; Baitella-Eberle, G.; Kag J. Biol. Chem. 260, 10032-10038, 1985
A;Title: (¹C,²H) metallothioneins from fetal bovine liver. Chemical and spectroscopic
A;Reference number: A92490; MUID:8526146; PMID:4019500
A;Accession: A23889
A;Molecule type: protein
A; Residues: 1-61 <MUN>
C; Superfamily: metallothionein

Query Match 15.7%; Score 61.5%; DB 2; Length 61;
Best Local Similarity 36.7%; Pred. No. 16;
Matches 18; Conservative 5; Mismatches 19; Indels 7; Gaps 4;

Qy 1 GGFGLGGRKCPNSEIFSRCDGR-CORFCPNVVKPLC1K1KAPGCYCR 49

Db 10 ggSCTAGSCCKA---CRCPs-CKKSCCCPVG-CAK-CAQGCVCK 51

RESULT 13
SRHUIA
metallothionein 1A - human

C:Species: Homo sapiens (man)
C:Date: 24-Jun-1987 #sequence_revision 09-Sep-1994 #text_change 22-Jun-1999
C:Accession: A24502
R:Richards, R.I.; Heguy, A.; Karin, M.

Cell, 37, 263-272, 1984
A:Title: Structural and functional analysis of the human metallothionein-1A gene: difference number: A24502; MUID:84205649; PMID:6327055
A:Accession: A24502

A: Molecule type: DNA
A: Residues: 1-61 <RC>
A: Cross-references: GB:K01383; NID:9187536; PIDN:AAA59586.1; PMID:9386864

C:Genetics: GDE:MT1A; MP1:125559; OMIM:156350
A:Cross-references: GDB:125559; OMIM:156350
A:Map position: 16q13-16q13

C:Superfamily: metallothionein
C:Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster;
F:1-29/Domain: beta <NH2>

F:30-61/Domain: alpha <ALP>
F:1/Modified site: acetylated amino end (Met) #status predicted

F:5,7,13,15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted
F:33,34,36,37,41,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status predicted

Query Match Best Local Similarity 15.5%; Score 60.5; DB 2; Length 61;
Matches 18; Conservative 2; Misnatches 21; Indels 13; Gaps 2;

Qy 7 GGRGKCPSENEIFSRCDGRQCRCPPNVPKPLCIKICAPGCCYRLNKKVC 60
Db 15 GGSCCKCSNCACTSCKKASCCDCPSGCSK-----CASGCYC-----KGKTC 55

RESULT 14
JC1449
metallothionein A - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C:Accession: JC1449; A27490; S16996; S15508
R:Hong, Y.; Schartl, M.

DNA 6, 519-528, 1987
Gene 120, 277-279, 1992
A:Title: Structure of the rainbow trout metallothionein A gene.
A:Reference number: JC1449; MUID:93013046; PMID:1398141
A:Accession: JC1449

A: Molecule type: DNA
A: Residues: 1-61 <RD>
A: Cross-references: GB:MB1800; NID:9213812; PIDN:AAA49564.1; PMID:9213815
R:Bonham, R.; Zafarullah, M.; Gedamu, L.

DNA 6, 519-528, 1987
Gene 120, 277-279, 1992
A:Title: The rainbow trout metallothioneins: molecular cloning and characterization of t

A:Reference number: A27490; MUID:89111026; PMID:2448099
A:Accession: A27490

A: Molecule type: mRNA
A: Residues: 1-61 <BON>
A: Cross-references: GB:MB1803; NID:9213814; PIDN:AAA49565.1; PMID:9213815
R:Kille, P.; Stephens, P.E.; Kay, J.

Biochim. Biophys. Acta 1089, 407-410, 1991
A:Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone lo

A:Reference number: S16996; MUID:91316146; PMID:185984
A:Accession: S16996

A: Molecule type: mRNA
A: Residues: 1-61 <KIL>
A: Cross-references: EMBL:X59395; NID:964330; PIDN:CAA42038.1; PMID:964331
C:Genetics:
A:Gene: 1M7-A
A:Introns: 9/1; 32/1

Result No.	Score	Query	Match	Length	DB ID	Description
1	104.5	26.7	56	1	AMCI_APIME	P5682 apis mellifera hemolymph
2	80.5	20.6	63	1	ICE1_ASCSU	P07851 acaris suum hemolymph
3	78.5	20.1	65	1	ICE2_ASCSU	P07852 acaris suum hemolymph
4	73	18.0	60	1	MT_PerfL	P52725 perca fluviatilis hemolymph
5	70.5	18.0	62	1	ITRL_ASCSU	P19398 acaris suum hemolymph
6	69	17.6	60	1	MTB_Orcmy	P09862 oncorhynchus tshawytscha hemolymph
7	69	17.6	60	1	MT_Esolu	P25127 esox lucius hemolymph
8	68	17.4	60	1	MT_PlRpl	P07216 pleuronectes americanus hemolymph
9	68	17.4	60	1	MT_Psram	P55945 pseudopleuronectes americanus hemolymph
10	67	17.1	62	1	MT4_HUMAN	P47944 homo sapiens hemolymph
11	66.5	17.0	61	1	MT_Balmy	O18842 balanoidae hemolymph
12	66	16.9	60	1	MTB_Salis	P52720 salmo salar hemolymph
13	65	16.6	60	1	MT_Zovavi	P52728 zoarcidae hemolymph
14	65	16.6	62	1	MT4_Mouse	P47945 mus musculus hemolymph
15	63.5	16.2	60	1	MT_Ambre	O42152 ambystoma tigrinum hemolymph
16	62.5	16.0	62	1	MT4_Canfa	O9tu15 canis familiaris hemolymph
17	62	15.9	62	1	MT2A_Rabbit	P18055 oryctolagus cuniculus hemolymph
18	62	15.9	62	1	MT2C_Rabbit	P80290 oryctolagus cuniculus hemolymph
19	61.5	15.7	61	1	MT1_BOVIN	P58280 bos taurus hemolymph
20	60.5	15.5	61	1	MT1_HUMAN	P04731 homo sapiens hemolymph
21	60.5	15.5	61	1	MT2_STECo	P14425 stenella coerulea hemolymph
22	60.5	15.5	61	1	MTA_ONCMY	P09861 oncorhynchus tshawytscha hemolymph
23	60	15.3	61	1	MT_PAGMA	P91bb50 pagrus major hemolymph
24	59.5	15.2	61	1	MT1_HUMAN	P07438 homo sapiens hemolymph
25	59.5	15.2	61	1	MT1_HUMAN	P09851 canis familiaris hemolymph
26	59.5	15.2	61	1	MT2_CANFA	P09852 canis familiaris hemolymph
27	59.5	15.2	62	1	MT2_CAEEL	P17512 caenorhabditis elegans hemolymph
28	59.5	15.2	63	1	MT1_COLLI	P15786 columba livia hemolymph
29	59	15.1	60	1	MTB_CHAAC	P52724 chaenocnephala hemolymph
30	59	15.1	60	1	MTB_CHATHA	O13259 chionodraco hemolymph
31	59	15.1	60	1	MTB_DICLIA	O9pb99 diceratrichia hemolymph
32	59	15.1	60	1	MTB_PAGBE	O93609 pagethenia hemolymph
33	59	15.1	60	1	MT_LIZAU	O13257 liza aurata hemolymph

ALIGNMENTS						
RESULT 1						
AMCI_APIME	STANDARD;	PRT;	56 AA.			
ID AMCI_APIME						
AC P5682;						
DT 15-JUL-1999 (Rel. 38, Created)						
DT 15-JUL-1999 (Rel. 39, Last sequence update)						
DT 30-MAY-2000 (Rel. 39, Last annotation update)						
DE Chymotrypsin Inhibitor (AMCI).						
OS Apis mellifera (Honeybee).						
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apocrita;						
NCBI_TaxID=7460;						
RN [1]						
RP SEQUENCE AND STRUCTURE BY NMR.						
RC TISSUE=hemolymph;						
RX MEDLINE=99339935; PubMed=10411628;						
RA Bania J., Stachowiak D., Polanowski A.;						
RT "Primary structure and properties of the cathepsin G/chymotrypsin inhibitor from the larval hemolymph of <i>Apis mellifera</i> ."						
RL Eur. J. Biochem. 262:650-68 (1999).						
CC -!- FUNCTION: CHYMOTRYPSIN G INHIBITOR.						
CC -!- SUBCELLULAR LOCATION: Secreted.						
DR PDB; 1CCV; 12-MAR-99.						
DR InterPro; IPB002919; TIL_Cysrich.						
DR Pfam; PF01826; TIL; 1.						
KW Serine protease inhibitor; 3D-structure.						
FT DISULFID 3 36						
FT DISULFID 12 32						
FT DISULFID 16 26						
FT DISULFID 20 56						
FT DISULFID 38 50						
SQ SEQUENCE 56 AA; 5973 MW; 092B2815AE6B2B7F CRC64+;						
Query Match Score 104.5% Best Local Similarity 36.83%; DB 1; Length 56;						
Matches 21; Conservative 21; Mismatches 26; Indels 3; Gaps 2;						
QY 11 KCPSNEIIFSRCDGRQRFCPNVVPKPK-LCIKICAPGVCRGLYLNKKVCPVRSKC 66						
Db 2 ECGPNEVENTGSACAPTCAQ-QPKTRCTMOCRICQCQEGFLRNREGACVLPNC 56						
RESULT 2						
ICEL_ASCSU	STANDARD;	PRT;	63 AA.			
ID ICE1_ASCSU						
AC P07851;						
DT 01-AUG-1988 (Rel. 08, Created)						
DT 01-AUG-1988 (Rel. 08, Last sequence update)						
DT 15-JUL-1999 (Rel. 39, Last annotation update)						
DE Chymotrypsin elastase isoinhibitor 1 (C/E-1 inhibitor).						
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).						
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;						
OC Ascarididae; Ascaris.						
NCBI_TaxID=6253;						
RN [1]						

RP SEQUENCE; PubMed=6564898;
 RX MEDLINE=84255715; PubMed=6564898;
 RA Babin D.R.; Peanasky R.J.; Goos S.M.;
 RT "The isoInhibitors of chymotrypsin/elastase from Ascaris
 lumbicoides: the primary structure";
 RL Arch. Biochem. Biophys. 232:143-161(1984).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
 RX MEDLINE=95006335; PubMed=7922044;
 RA Huang K.; Strnadka N.C.; Bernard V.D.; Peanasky R.J.; James M.N.;
 RT "The molecular structure of the complex of Ascaris
 chymotrypsin/elastase inhibitor with porcine elastase.";
 RT Structure 2:679-689(1994).
 RL -!- FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES.
 CC -!- SIMILARITY: BELONGS TO THE ASCARIS TRYPsin INHIBITOR FAMILY.
 DR PIR: S07127; S07127.
 DR PDB: 1EAI; 05-APR-95.
 DR InterPro; IPR00919; TIL_Cysrich.
 DR Pfam; PF01826; TIL_1.
 KW Serine protease inhibitor; 3D-structure.
 FT DISULFID 5 38
 FT DISULFID 14 33
 FT DISULFID 17 29
 FT DISULFID 21 60
 FT DISULFID 40 54
 FT ACT SITE 31 32 REACTIVE BOND.
 SQ SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;
 Score 80.5; DB 1; Length 63;
 Best Local Similarity 20.6%; Pred. No. 0.029;
 Matches 20; Conservative 30.3%; Indels 13; Gaps 4;
 Mismatches 23;
 ID ICB2_ASCSU STANDARD; PRT; 65 AA.
 AC P07852;
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DR Chymotrypsin/elastase isoInhibitors 2 to 5.
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
 OC Ascaridae; Ascaris.
 OC NCBI_TAXID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84255715; PubMed=6564898;
 RA Babin D.R.; Peanasky R.J.; Goos S.M.;
 RT "The isoInhibitors of chymotrypsin/elastase from Ascaris
 lumbicoides: the primary structure";
 RL Arch. Biochem. Biophys. 232:143-161(1984).
 CC -!- SIMILARITY: BELONGS TO THE ASCARIS TRYPSIN INHIBITOR FAMILY.
 DR HSSP; P07851; 1EAI.
 DR InterPro; IPR00919; TIL_Cysrich.
 DR Pfam; PF01826; TIL_1.
 KW Serine protease inhibitor.
 FT DISULFID 4 37 BY SIMILARITY.
 FT DISULFID 13 32 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 20 59 BY SIMILARITY.
 FT DISULFID 39 53 BY SIMILARITY.
 FT ACT SITE 31 32 REACTIVE BOND.
 FT VARIANT 25 25 K->N (IN INHIBITOR 2 AND 4).
 FT VARIANT 40 40 T->S (IN INHIBITOR 2 AND 4).
 FT VARIANT 64 65 MISSING (IN INHIBITOR 2).
 FT VARIANT 65 65 K->E (IN INHIBITOR 3).
 FT VARIANT 65 65 K->R.
 SQ SEQUENCE 65 AA; 7241 MW; B4E5ICA166BA4BE3 CRC64;
 Query Match 20.1%; Score 78.5; DB 1; Length 65;
 Best Local Similarity 31.7%; Pred. No. 0.048;
 Matches 19; Conservative 6; Mismatches 32; Indels 3; Gaps 2;
 ID MT_PEREL STANDARD; PRT; 60 AA.
 AC P52725;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Metallothionein (MT).
 GN MT.
 OS Perca fluviatilis (Perch).
 OC Eukaryota; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Perciformes; Percidae;
 OC Percidae; Perca.
 RN [1] TexID=8166;
 RN SEQUENCE FROM N.A.
 RC Kille P.; Olson P.E.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: METALLOTHIONEPINS HAVE A HIGH CONTENT OF CYSTEINE.
 CC -!- RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINY THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
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RESULT 4
 ID MT_PEREL STANDARD; PRT; 60 AA.
 AC P52725;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein (MT).
 GN MT.
 OS Perca fluviatilis (Perch).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Perciformes; Percidae;
 OC Percidae; Perca.
 RN [1] TexID=8166;
 RN SEQUENCE FROM N.A.
 RC Kille P.; Olson P.E.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: METALLOTHIONEPINS HAVE A HIGH CONTENT OF CYSTEINE.
 CC -!- RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINY THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
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CC EMBL; X97272; CAA65927; 1; -.
 DR HSSP; P25184; 1J19.
 DR InterPro; IPR003019; Metallothionein.
 DR InterPro; IPR000006; Metallothionein_vert.
 PFam; PF00131; metalthio_1.
 DR PRINTS; PRO0860; MYVERSEBRATE.
 DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster.
 DR DOMAIN 1 1 ALPHA.
 FT DOMAIN 29 60 BETA.
 FT METAL 4 4 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 14 14 CLUSTER B.
 FT METAL 18 18 CLUSTER B.
 FT METAL 20 20 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 32 32 CLUSTER A.
 FT METAL 33 33 CLUSTER A.

DR PIR; S16997; S16997.
 DR PIR; S15509; S15509.
 DR HSSP; P28184; IJF9.
 DR InterPro; IPR003019; Metallothionein.
 DR InterPro; IPR000006; Metallothionein_vrt.
 DR Pfam; PF00131; metallothio; 1.
 DR PRINTS; PRO0860; MIVERTERATE.
 DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 FW Metal-binding; Metal-thiolate cluster.
 FT DOMAIN 1 28 BETA.
 FT DOMAIN 29 60 ALPHA.
 FT DOMAIN 4 4 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 14 14 CLUSTER B.
 FT METAL 18 18 CLUSTER B.
 FT METAL 20 20 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 32 32 CLUSTER A.
 FT METAL 33 33 CLUSTER A.
 FT METAL 35 35 CLUSTER A.
 FT METAL 36 36 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 43 43 CLUSTER A.
 FT METAL 47 47 CLUSTER A.
 FT METAL 49 49 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 58 58 CLUSTER A.
 FT METAL 59 59 CLUSTER A.
 SQ SEQUENCE 60 AA; 6033 MW; 9EA1E7@FB59B4EE CRC64;

Query Match Score 69; DB 1; Length 60;
 Best Local Similarity 37.0%; Pred. No. 0.46;
 Matches 20; Conservative 2; Mismatches 18; Indels 14; Gaps 3;

Qy 7 GGRGKCPSENEFSRCDGRQCQFCPNVVKPLCICIKCAPGCVCRGLYRLNIKKYVC 60
 Db 15 GGSKCKC-SNCACTSCKSKCCCPSDCSK-----CAGSCVC-----KGKTC 54

RESULT 7
 MT_ESOLU STANDARD PRT; 60 AA.
 ID MT_ESOLU
 AC P25127;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein (MT).
 GN Esox lucius (Northern pike).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
 OC Esocidae; Esox.
 NCBI_TaxID=8010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 MEDLINE=91316146; PubMed=1859844;
 RX Kille P., Stephens P.E., Ray J.;
 RA "Elucidation of cDNA sequences for metallothionein genes in rainbow trout, stone loach and pike liver using the polymerase chain reaction";
 RT Blochim. Biophys. Acta 1089:407-410(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=94032489; PubMed=8218416;
 RX Kille P., Ray J., Sweeney G.E.;
 RA "Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant fish (pike and stone loach)." ;
 RT Blochim. Biophys. Acta 1216:55-64 (1993).
 RL Euperonectes platessa (Plaice).
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE

CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYLY THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY: FAMILY 1.
 CC

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 CC

CC DR EMBL; X59392; CAA42035; 1;
 CC DR EMBL; X70042; CAA49636; 1;
 CC DR PIR; S17175; S17175.
 CC DR PIR; S15503; S15503;
 CC DR PIR; S38334; S38334.
 CC DR PIR; S31723; S31723.
 CC DR HSSP; P02795; 1MHU.
 CC DR InterPro; IPR03019; Metallothionein.
 CC DR InterPro; IPR00006; Metallothionein_vrt.
 CC DR Pfam; PF01311; metallothio; 1.
 CC DR PRINTS; PRO0060; MIVERTERATE.
 CC DR PROSITE; PS00203; METALLOTHIONEINE_VRT; 1.
 CC KW Metal-binding; Metal-thiolate cluster.
 CC FT DOMAIN 1 28 BETA.
 CC FT DOMAIN 29 60 ALPHA.
 CC FT DOMAIN 30 4 CLUSTER B.
 CC FT DOMAIN 31 6 CLUSTER B.
 CC FT DOMAIN 32 6 CLUSTER B.
 CC FT DOMAIN 33 12 CLUSTER B.
 CC FT DOMAIN 34 14 CLUSTER B.
 CC FT DOMAIN 35 18 CLUSTER B.
 CC FT DOMAIN 36 20 CLUSTER B.
 CC FT DOMAIN 37 23 CLUSTER B.
 CC FT DOMAIN 38 23 CLUSTER B.
 CC FT DOMAIN 39 25 CLUSTER B.
 CC FT DOMAIN 40 28 CLUSTER B.
 CC FT DOMAIN 41 32 CLUSTER B.
 CC FT DOMAIN 42 33 CLUSTER B.
 CC FT DOMAIN 43 35 CLUSTER B.
 CC FT DOMAIN 44 35 CLUSTER B.
 CC FT DOMAIN 45 36 CLUSTER B.
 CC FT DOMAIN 46 40 CLUSTER B.
 CC FT DOMAIN 47 43 CLUSTER B.
 CC FT DOMAIN 48 44 CLUSTER B.
 CC FT DOMAIN 49 46 CLUSTER B.
 CC FT DOMAIN 50 47 CLUSTER B.
 CC FT DOMAIN 51 49 CLUSTER B.
 CC FT DOMAIN 52 50 CLUSTER B.
 CC FT DOMAIN 53 52 CLUSTER B.
 CC FT DOMAIN 54 54 CLUSTER B.
 CC FT DOMAIN 55 55 CLUSTER B.
 CC FT DOMAIN 56 56 CLUSTER B.
 CC FT DOMAIN 57 58 CLUSTER B.
 CC FT DOMAIN 58 58 CLUSTER B.
 CC FT DOMAIN 59 59 CLUSTER B.
 CC SQ SEQUENCE 60 AA; 59.9 MW; 9EA1E43P9F8D97E CRC64;

Query Match Score 69; DB 1; Length 60;
 Best Local Similarity 37.0%; Pred. No. 0.46;
 Matches 20; Conservative 2; Mismatches 18; Indels 14; Gaps 3;

Qy 7 GGRGKCPSENEFSRCDGRQCQFCPNVVKPLCICIKCAPGCVCRGLYRLNIKKYVC 60
 Db 15 GGSKCKC-SNCACTSCKSKCCCPSDCSK-----CAGSCVC-----KGKTC 54

RESULT 8
 MT_PLEPL STANDARD PRT; 60 AA.
 ID MT_PLEPL
 AC P07216;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein (MT).
 GN MT
 OS Pleuronectes platessa (Plaice).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Esociformes;
 OC Esocidae; Esox.
 NCBI_TaxID=8010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 MEDLINE=91316146; PubMed=1859844;
 RX Kille P., Stephens P.E., Ray J.;
 RA "Elucidation of cDNA sequences for metallothionein genes in rainbow trout, stone loach and pike liver using the polymerase chain reaction";
 RT Blochim. Biophys. Acta 1089:407-410(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=94032489; PubMed=8218416;
 RX Kille P., Ray J., Sweeney G.E.;
 RA "Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant fish (pike and stone loach)." ;
 RT Blochim. Biophys. Acta 1216:55-64 (1993).
 RL Euperonectes platessa (Plaice).
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE

Query Match Score 69; DB 1; Length 60;
 Best Local Similarity 35.2%; Pred. No. 0.46;
 Matches 19; Conservative 3; Mismatches 18; Indels 14; Gaps 3;

Qy 7 GGRGKCPSENEFSRCDGRQCQFCPNVVKPLCICIKCAPGCVCRGLYRLNIKKYVC 60
 Db 15 GGSKCKC-SNCACTSCKSKCCCPSDCSK-----CAGSCVC-----KGKTC 54

RESULT 9						
MT_PSPAM	MT_PSPAM	STANDARD;	PRT;	60 AA.		
ID	AC	P55945;				
AC	DT	01-NOV-1997 (Rel. 35, Created)				
DT	DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	DE	Metallothionein (MT).				
GN	OS	Pseudopleuronectes americanus (Winter flounder) (Pleuronectes americanus).				
RA	RC	TISSUE="Liver;				
RA	RA	Chan K.-M., Davidson W.S., Hew C.-L., Fletcher G.L.; "Molecular cloning of metallothionein cDNA and analysis of metallothionein gene expression in winter flounder tissues." Can. J. Zool. 67:2520-2527 (1989).				
RT	RL	-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).				
CC	CC	-!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS AND ARE COORDINATED VIA CYSTEINY THIOLATE BRIDGES TO CYSTEINE LIGANDS. -CLUSTER B, THE CORRESPONDING REGION WITHIN CC				
CC	CC	BETA DOMAIN CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES. -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAM HSSP_P28184; LJ19.				
DR	DR	InterPro: IPR003019; Metallothionein.				
DR	DR	InterPro: IPR000006; Metallothionein.				
DR	DR	pfam: PF00131; metalthio_1.				
PRINTS:	PRINTS:	PRO0080: MIVERTEREBRATE.				
KW	KW	PROSITE: PS0003; METALLOTHIONEIN_VRT; 1. Metal-binding Metal-thiolate cluster; Copper; Acetylation.				
FT	MOD_RES	1 1				
FT	DOMAIN	1 1				
FT	DOMAIN	1 28				
FT	DOMA IN	29 60				
FT	METAL	4 4				
FT	METAL	6 6				
FT	METAL	12 12				
FT	METAL	14 14				
FT	METAL	18 18				
FT	METAL	20 20				
FT	METAL	23 23				
FT	METAL	25 25				
FT	METAL	28 28				
FT	METAL	32 32				
FT	METAL	33 33				
FT	METAL	35 35				
FT	METAL	36 36				
FT	METAL	40 40				
FT	METAL	43 43				
FT	METAL	47 47				
FT	METAL	49 49				
FT	METAL	54 54				
FT	METAL	58 58				
SQ	SEQUENCE	60 AA: 6043 MW:				
Query Match	17.4%	Score 68; DB 1; Length 60;				
Best Local Similarity	35.28;	Pred. No. 0.58;				
Matches 19;	Conservative	3; Mismatches 18; Indels 14;				
OY	7	GGRGKCPSPSNEIFSRCDGRQRFQPNVVKPLKIKTCAPCVCRLGYLERNKKVKG 60				

RESULT 10	T4_HUMAN	STANDARD;	PRT;	62 AA.
	MT4_HUMAN			
	C			
	PA-T			
01-FEB-1996	(Rel. 33, Created)			
01-FEB-1996	(Rel. 33, Last sequence update)			
15-JUN-2002	(Rel. 41, Last annotation update)			
Metallothionein-IV (MT-IV).				
MT4.				
Homo sapiens (Human).	Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. N			
NCBI_TaxID=9606;				
[1]	SEQUENCE FROM N.A.			
X	MEDLINE=9421779; PubMed=8003488;			
X	Quafe C.J., Findley S.D., Erickson J.C., Froelick G.J., Kelly E.J., Zambrowicz B.P., Palmiter R.D.;			
A	"Induction of a new metallothionein isoform (MT-IV) occurs during differentiation of stratified squamous epithelia.";			
A	Biochemistry 33:7250-7259(1994).			
- - FUNCTION: SEEKS TO BIND ZINC AND COPPER. COULD PLAY A SPECIAL ROLE IN REGULATING ZINC METABOLISM DURING THE DIFFERENTIATION OF STRATIFIED EPITHELIAL.				
- - SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.				
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EMBL; U07807; AAA2023.2.1; -.				
HSSP; P1005; 1MRB.				
InterPro; IPR000006; Metallothionein.				
InterPro; IPR000006; Metallothionein_vrt.				
pfam; PF00131; metalthio.1.				
PRINTS; PRO0860; MTVERTEBRATE.				
PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.				
Metal-binding; Metal-thiolate cluster; Zinc; Copper.				
METAL	6	6	CLUSTER B (BY SIMILARITY).	
METAL	8	8	CLUSTER B (BY SIMILARITY).	
METAL	14	14	CLUSTER B (BY SIMILARITY).	
METAL	16	16	CLUSTER B (BY SIMILARITY).	
METAL	20	20	CLUSTER B (BY SIMILARITY).	
METAL	22	22	CLUSTER B (BY SIMILARITY).	
METAL	25	25	CLUSTER B (BY SIMILARITY).	
METAL	27	27	CLUSTER B (BY SIMILARITY).	
METAL	30	30	CLUSTER B (BY SIMILARITY).	
METAL	34	34	CLUSTER A (BY SIMILARITY).	
METAL	35	35	CLUSTER A (BY SIMILARITY).	
METAL	37	37	CLUSTER A (BY SIMILARITY).	
METAL	38	38	CLUSTER A (BY SIMILARITY).	
METAL	42	42	CLUSTER A (BY SIMILARITY).	
METAL	45	45	CLUSTER A (BY SIMILARITY).	
METAL	49	49	CLUSTER A (BY SIMILARITY).	
METAL	51	51	CLUSTER A (BY SIMILARITY).	
METAL	58	58	CLUSTER A (BY SIMILARITY).	
METAL	60	60	CLUSTER A (BY SIMILARITY).	
METAL	61	61	CLUSTER A (BY SIMILARITY).	
SEQUENCE	62 AA;	6419 MW;	36157CBA17BF28CC C9G64;	
SQL				
Query Match	17.1%	Score 67; DB 1;	Length 62;	
Best Local Similarity	35.1%	Pred. No. 0.76;		
Matches 20;	Conservative 8;	Mismatches 23;	Indels 6;	Gaps 4;
RESULT 11	MT-BALMY	STANDARD;	PRT;	61 AA.
	ID MT_BALMY			
	AC O18842;			
	DT 16-OCT-2001 (Rel. 40, Created)			
	DT 16-OCT-2001 (Rel. 40, Last sequence update)			
	DT 15-JUN-2002 (Rel. 41, Last annotation update)			
	DT Metallothionein (MT).			
	OS Balaena mysticetus (Bowhead whale).			
	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	OC N			
	NCBI_TaxID=27602;			
	OX NCBI_TaxID=27602;			
RN [1]	SEQUENCE FROM N.A.			
RP TISSUE-Liver;				
RC Kayser J., O'Hara T., Goodwin T., Linnehan R., Hammond T.;				
RA Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.				
RL -1: FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).				
CC -1: SUBUNIT: MONOMER (BY SIMILARITY).				
CC -1: DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOATE BRIDGES TO 11 CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.				
CC -1: SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.				
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CC	EMBL; A022117; AB72006.1; -.			
CC HSSP; P02795; 2MIU.				
DR InterPro; IPR003019; Metallothionein.				
DR InterPro; IPR000006; metalthio.1.				
DR Pfam; PF00131; metalthio.				
DR PRINTS; PRO0860; MTVERTEBRATE.				
DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.				
KW Metal-binding; Metal-thiolate cluster; Acetylation.				
KW DOMAIN	1	29	BETA.	
FT DOMAIN	1	61	ALPHA.	
FT METAL	5	5	CLUSTER B (BY SIMILARITY).	
FT METAL	7	7	CLUSTER B (BY SIMILARITY).	
FT METAL	13	13	CLUSTER B (BY SIMILARITY).	
FT METAL	15	15	CLUSTER B (BY SIMILARITY).	
FT METAL	19	19	CLUSTER B (BY SIMILARITY).	
FT METAL	21	21	CLUSTER B (BY SIMILARITY).	
FT METAL	24	24	CLUSTER B (BY SIMILARITY).	
FT METAL	26	26	CLUSTER B (BY SIMILARITY).	
FT METAL	29	29	CLUSTER B (BY SIMILARITY).	
FT METAL	33	33	CLUSTER A (BY SIMILARITY).	
FT METAL	34	34	CLUSTER A (BY SIMILARITY).	
FT METAL	36	36	CLUSTER A (BY SIMILARITY).	
FT METAL	37	37	CLUSTER A (BY SIMILARITY).	
FT METAL	41	41	CLUSTER A (BY SIMILARITY).	
FT METAL	44	44	CLUSTER A (BY SIMILARITY).	
FT METAL	48	48	CLUSTER A (BY SIMILARITY).	
FT METAL	50	50	CLUSTER A (BY SIMILARITY).	
FT METAL	57	57	CLUSTER A (BY SIMILARITY).	
FT METAL	59	59	CLUSTER A (BY SIMILARITY).	
FT METAL	60	60	CLUSTER A (BY SIMILARITY).	
SO SEQUENCE	61 AA;	6025 MW;	4D0AC5ECD2AA3 CRC64;	

Query Match 17.0%; Score 66.5.; DB 1; Length 61;
 Best local Similarity 38.8%; Pred. No. 0.85;
 Matches 19; Conservative 2; Mismatches 21; Indels 7; Gaps 3;

FT METAL 58 58 CLUSTER A.
 FT METAL 59 59 CLUSTER A.
 SQ SEQUENCE 60 AA; 5959 MW; 187A0D0FB5BD967 CRC64;

Query Match 16.9%; Score 66.; DB 1; Length 60;
 Best Local Similarity 35.2%; Pred. No. 0.95;
 Matches 19; Conservative 3; Mismatches 18; Indels 14; Gaps 3;

FT METAL 58 59 CLUSTER A.
 FT METAL 59 59 CLUSTER A.

QY 1 GGFGGLGGRKCPNSNETFSRCDGRCQREFCPNVPKLICIKICAPGVCR 49
 DB 10 GGSCTCAGSCKCKECKCTS-CKKSCCCP---PGCTK-CAQGCVCVK 51

RESULT 1.2
 ID MTB_SALSA STANDARD PRT; 60 AA.
 AC P5720;
 DE Metallothionein B (MT-B).
 GN MTB.
 OS Salmo salar (Atlantic salmon). Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Pctacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 RN [1]TaxID=8030;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Kille P., Olson P.E.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC -1- RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS;
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOATE BRIDGES TO 11
 CC CYSTEINE LIGANDS CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC -1- SIMILARITY: CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC
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 CC -1- BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC
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 CC -1- BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC
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 CC -1- BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC
 DR X97270; CAA65930; 1. DR HSSP: P28184; LJ19.
 DR HSSP; P28184; LJ19.
 DR InterPro; IPR03019; Metallothion.
 DR InterPro; IPR00006; Metallothio_vrt.
 DR Pfam; PF00131; metalthio_1.
 DR PRINTS; PRO0860; MVERTERBRATE.
 DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster.
 FT DOMAIN 1 28 BETA.
 FT DOMAIN 29 60 ALPHA.
 FT METAL 4 4 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 14 14 CLUSTER B.
 FT METAL 18 18 CLUSTER B.
 FT METAL 20 20 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 32 32 CLUSTER A.
 FT METAL 33 33 CLUSTER A.
 FT METAL 35 35 CLUSTER A.
 FT METAL 36 36 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 43 43 CLUSTER A.
 FT METAL 47 47 CLUSTER A.
 FT METAL 49 49 CLUSTER A.
 FT METAL 54 54 CLUSTER A.

RESULT 1.3
 ID MT_ZOAVI STANDARD PRT; 60 AA.
 AC P52738;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metallothionein (MT).
 GN MT.
 OS Zoarcidae:Zoarcidae:zoarcidae:
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Zoarcidae:
 OC Zoarcidae:Zoarcidae:
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Kille P., Olsson P.E.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC -1- RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS;
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOATE BRIDGES TO 11
 CC CYSTEINE LIGANDS CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC -1- SIMILARITY: CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC
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 CC -1- BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC
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 CC -1- BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
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 CC -1- BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
 CC
 DR EMBL; X97270; CAA65930; 1; -.
 DR HSSP: P28184; LJ19.
 DR InterPro; IPR03019; Metallothion.
 DR InterPro; IPR00006; Metallothio_vrt.
 DR Pfam; PF00131; metalthio_1.
 DR PRINTS; PRO0860; MVERTERBRATE.
 DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster.
 FT DOMAIN 1 28 BETA.
 FT DOMAIN 29 60 ALPHA.
 FT METAL 4 4 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 14 14 CLUSTER B.
 FT METAL 18 18 CLUSTER B.
 FT METAL 20 20 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 32 32 CLUSTER A.
 FT METAL 33 33 CLUSTER A.
 FT METAL 35 35 CLUSTER A.
 FT METAL 36 36 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 43 43 CLUSTER A.
 FT METAL 47 47 CLUSTER A.
 FT METAL 49 49 CLUSTER A.
 FT METAL 54 54 CLUSTER A.

Query Match 16 6%; Score 65; DB 1; Length 60;
Best Local Similarity 31.0%; Pred. No. 1.2;
Matches 20; Conservative 3; Mismatches 17; Indels 14; Gaps 4;

Qy 7 GGRKPSNEIFSRCDGRCQRFCPNVVKPLAKTICAPGVCRGLYLNKKV 60
Db 15 GGSCCK-TNCSTCKKSCCPGSG-----CTK-CASGCCV-----KGTC 54

RESULT 14

MT4_MOUSE
ID MT4_MOUSE
AC P47955;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metallothionein-IV (MT-IV).
GN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Quaife C.J., Findley S.D., Erickson J.C., Froelick G.J.,
RA Kelly E.J., Zambrowicz B.P., Palmer R.D.;
RT "Induction of a new metallothionein isoform (MT-IV) occurs during
RT differentiation of stratified squamous epithelia.";
RL Biochemistry 33:725-729 (1994).
RT FUNCTION: SEEMS TO BIND ZINC AND COPPER. COULD PLAY A SPECIAL ROLE
CC IN REGULATING ZINC METABOLISM DURING THE DIFFERENTIATION OF
CC STRATIFIED EPITHELIA.
CC TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN STRATIFIED SQUAMOUS
CC EPITHELIA ASSOCIATED WITH ORAL EPITHELLIA, OESOPHAGUS, UPPER
CC STOMACH, TAIL, FOOTPADS, AND NEONATAL SKIN. SUPERFAMILY: FAMILY 1.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.

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EMBL: U07608; AAA20233.1; -
DR HSSP; P18055; IMRb.
DR MGI:59692; Mt4.
DR InterPro; IPR003019; Metallothionein.
DR InterPro; IPR000006; Metlthion_vert.
PFam; PF00131; metlthio; 1.
PRINTS; PR00860; MINVERTERBATE.
KW Metal-binding; Metal-thiolate cluster; Zinc; Copper.
DR PROSITE; PS00203; METALLOTHIONEIN_VPT; 1.
FT METAL 6 6 CLUSTER B (BY SIMILARITY).
FT METAL 8 8 CLUSTER B (BY SIMILARITY).
FT METAL 14 14 CLUSTER B (BY SIMILARITY).
FT METAL 16 16 CLUSTER B (BY SIMILARITY).
FT METAL 20 20 CLUSTER B (BY SIMILARITY).
FT METAL 22 22 CLUSTER B (BY SIMILARITY).
FT METAL 25 25 CLUSTER B (BY SIMILARITY).
FT METAL 27 27 CLUSTER B (BY SIMILARITY).
FT METAL 30 30 CLUSTER B (BY SIMILARITY).
FT METAL 34 34 CLUSTER A (BY SIMILARITY).
FT METAL 35 35 CLUSTER A (BY SIMILARITY).
FT METAL 37 37 CLUSTER A (BY SIMILARITY).
FT METAL 38 38 CLUSTER A (BY SIMILARITY).
FT METAL 42 42 CLUSTER A (BY SIMILARITY).
FT METAL 45 45 CLUSTER A (BY SIMILARITY).
FT METAL 49 49 CLUSTER A (BY SIMILARITY).
FT METAL 51 51 CLUSTER A (BY SIMILARITY).
FT METAL 58 58 CLUSTER A (BY SIMILARITY).
FT METAL 60 60 CLUSTER A (BY SIMILARITY).
FT METAL 61 61 CLUSTER A (BY SIMILARITY).
SQ SEQUENCE 62 AA; 6276 MN; 8F78D46D0744333A CRC64;

Query Match 16 6%; Score 65; DB 1; Length 62;
Best Local Similarity 33.9%; Pred. No. 1.2;
Matches 21; Conservative 4; Mismatches 27; Indels 10; Gaps 4;

RESULT 15

MT_AMBBM
ID MT_AMBBM
AC 042152;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Metallothionein (MT) (Annot.).
GN MT-A.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metacozia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Ambystomatoidea; Ambystoma; Ambystoma;
OC Ambystoma.
RN [1]
RP SEQUENCE FROM N.A.
RC TISUSe-Embryo;
RX MEDLINE=98127743; PubMed=9468225;
RX MEDLINE=8296; NCBI_TAXID=8296;
RN [1]
RP Sequence FROM N.A.
RC
RA Saint-Jacques E., Guy J., Wirsanen L., Huard V., Stewart G.,
RA Seguin C.;
RT "Cloning of a complementary DNA encoding an Ambystoma mexicanum
RT metallothionein, Ammt, and expression of the gene during early
RL DNA Cell Biol. 17:83-91 (1998).
CC FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
CC "INDICATIONS FOR COMMERCIAL USE":
CC -!- DOMAIN: CLASS I METALLOTHIONEINES CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHEATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
CC

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CC DR AF00853; AAB71835.1; -
CC DR HSSP; P02795; 1MHU.
CC DR InterPro; IPR030319; Metallothionein.
CC DR InterPro; IPR000006; Metlthion_vert.
CC DR PRINTS; PR00860; MINVERTERBATE.
CC DR PROSITE; PS00203; METALLOTHIONEIN_VPT; 1.
CC FT METAL 6 6 CLUSTER B (BY SIMILARITY).
CC FT METAL 8 8 CLUSTER B (BY SIMILARITY).
CC FT METAL 14 14 CLUSTER B (BY SIMILARITY).
CC FT METAL 16 16 CLUSTER B (BY SIMILARITY).
CC FT METAL 20 20 CLUSTER B (BY SIMILARITY).
CC FT METAL 22 22 CLUSTER B (BY SIMILARITY).
CC FT METAL 25 25 CLUSTER B (BY SIMILARITY).
CC FT METAL 27 27 CLUSTER B (BY SIMILARITY).
CC

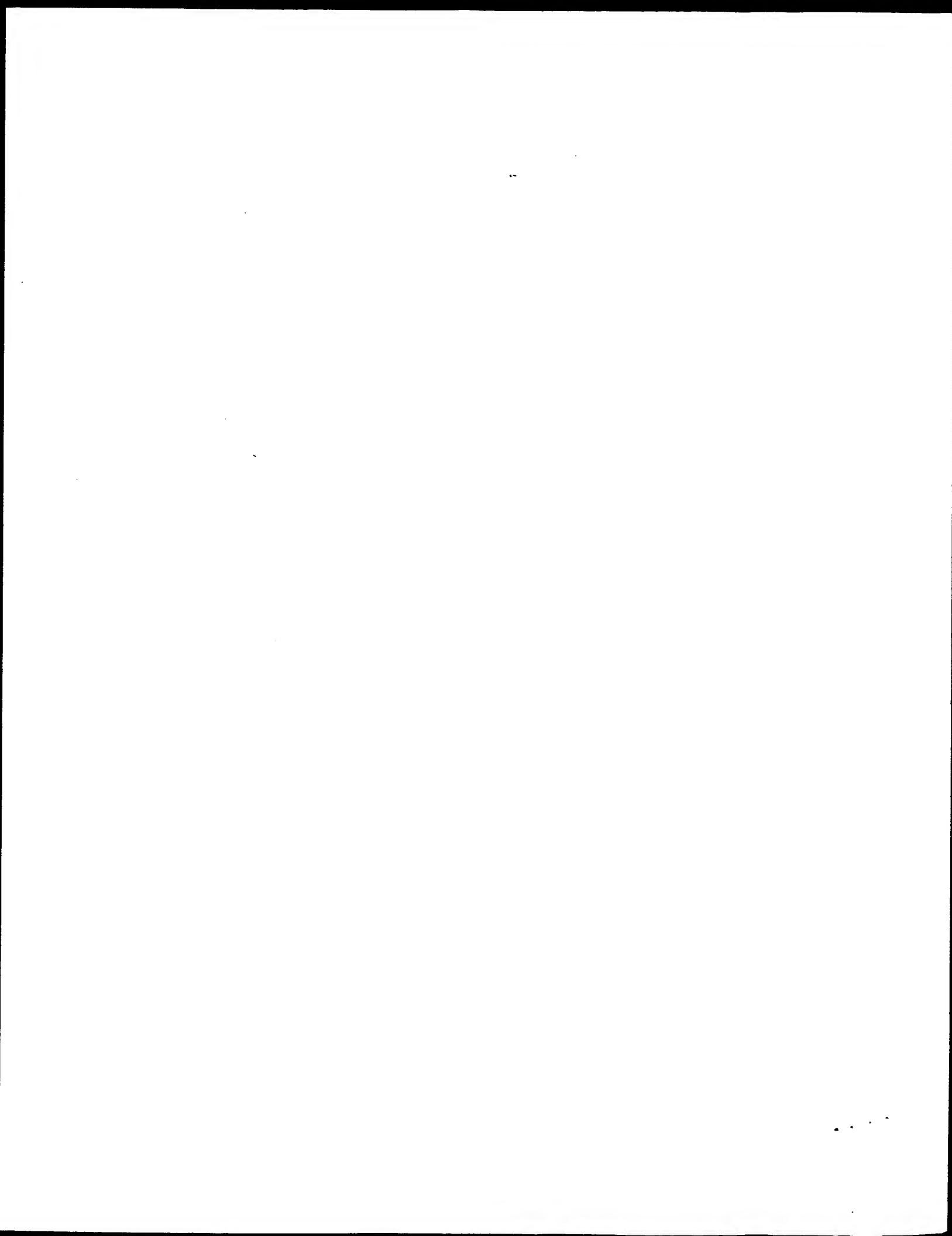
DR PRINTS; PRO0860; MIVERTEBRATE.
 DR PROSITE; PS00203; METALOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster.

FT DOMAIN	1	28	BETA
FT DOMAIN	29	60	ALPHA.
FT METAL	3	3	CLUSTER B.
FT METAL	5	5	CLUSTER B.
FT METAL	11	11	CLUSTER B.
FT METAL	13	13	CLUSTER B.
FT METAL	17	17	CLUSTER B.
FT METAL	19	19	CLUSTER B.
FT METAL	22	22	CLUSTER B.
FT METAL	24	24	CLUSTER B.
FT METAL	27	27	CLUSTER B.
FT METAL	31	31	CLUSTER A.
FT METAL	32	32	CLUSTER A.
FT METAL	34	34	CLUSTER A.
FT METAL	35	35	CLUSTER A.
FT METAL	39	39	CLUSTER A.
FT METAL	42	42	CLUSTER A.
FT METAL	46	46	CLUSTER A.
FT METAL	48	48	CLUSTER A.
FT METAL	56	56	CLUSTER A.
FT METAL	58	58	CLUSTER A.
SQ SEQUENCE	60 AA;	5979 MW;	AB05F491539532279 CRC64;

Query Match 16.2%; Score 63.5; DB 1; Length 60;
 Best Local Similarity 33.3%; Pred. No. 1.7;
 Matches 17; Conservative 4; Mismatches 23; Indels 7; Gaps 2;

Qy 1 GGFGGLGGRKPSNBFISRDGRCORFCPNVPKPLC1KICAPCCVCRIG 51
 Db 8 GGSCSCAGSCKCENCKCTS -CKKSCCSCCFSECEK-----CGQGCVCTGG 51

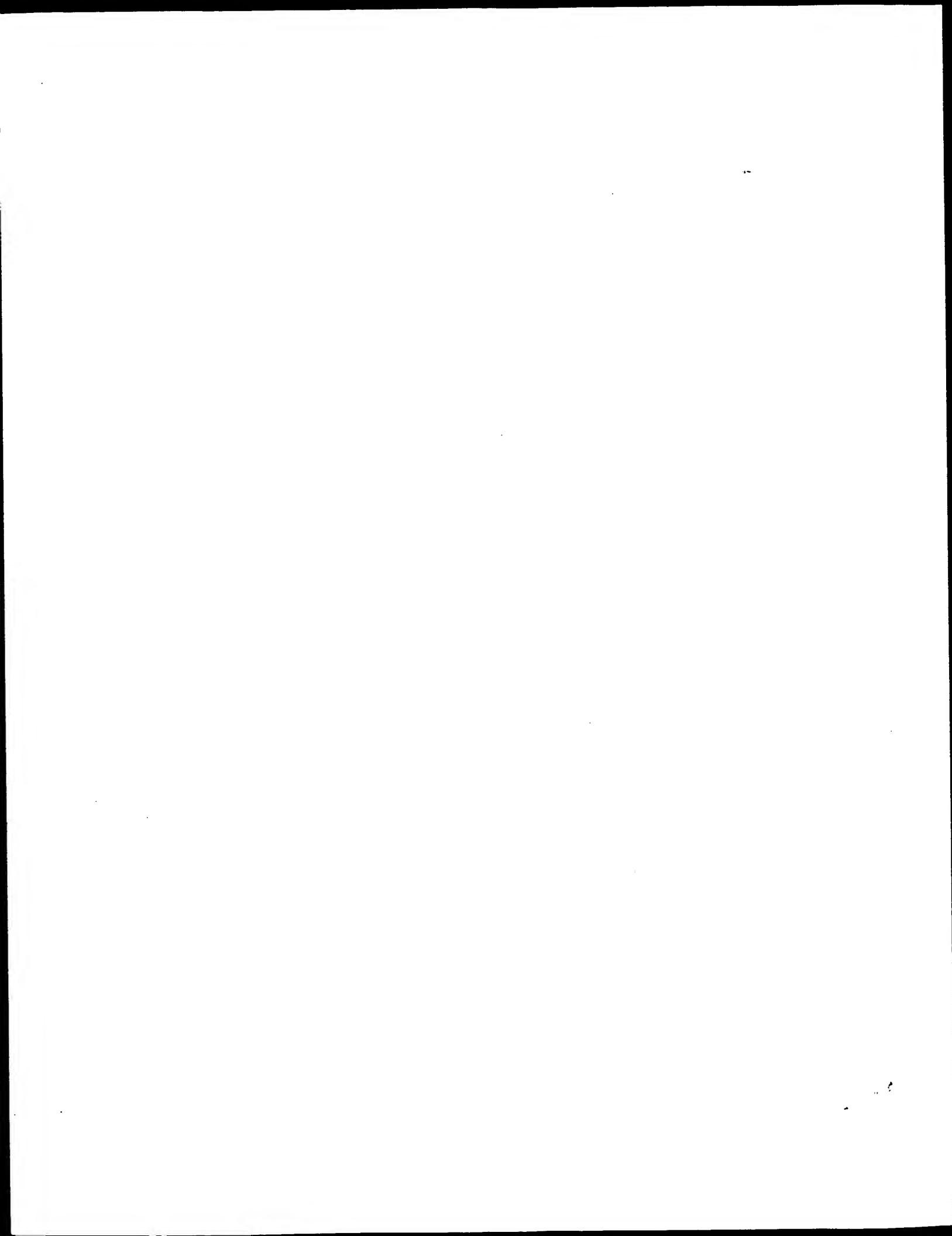
Search completed: February 26, 2003, 15:10:59
 Job time : 14 secs



•	Copyright (c) 1993 - 2003 Compugen Ltd.	GenCore version 5.1.3	4	Q8TC51
1	protein - protein search, using sw model			
on on:	February 26, 2003, 15:08:52 ; Search time 91 Seconds (without alignments)	151.705 Million cell updates/sec		
title:	US-09-506-978-1			
perfect score:	391			
sequence:	1 GFGGLGGRKGCPNSEIFSR CRLGYLRNKKVCKVPRSKCG 67			
scoring table:	BLOSUM62			
GapOp:	10.0 , Gapext 0.5			
searched:	671580 seqs, 206047115 residues			
total number of hits satisfying chosen parameters:	56343			
minimum DB seq length: 0				
maximum DB seq length: 67				
last-processing: Minimum Match 0 ₈				
Maximum Match 100 ₈				
Listing first 45 summaries				
Q8TC51 homo sapien				
Q9N9H1 ruditapes d				
Q8Y918 Picea maria				
Q8YUR2 anabena sp				
Q8TNN8 mechanosarc				
Q95P38 homerus ame				
Q95U91 scylla serr				
Q8ZK16 salmonella				
Q97BH4 thermoplasm				
Q9u623 pacifastacu				
Q95u93 portunus pe				
Q95u92 erlicheir s				
Q9Twf8 anemonia su				
Q9s8d2 cucumis mel				
Q77625 bos taurus				
Q9udp7 homo sapien				
Q9hj78 thermoplasm				
Q9qx87 ratites norv				
Q9twf8 anemonia su				
Q9hgh2 venerupis (
Q9bxg3 homo sapien				
Q18780 ovis aries				
Q9pv6 xiphophorus				
Q9ngh2 venerupis p				
Q9iy8 drosophila				
Q93gh5 bacillus su				
Q9bjk0 bactrocerida				
Q95p50 helix pomat				
Q90783 gallus gall				
Q60413 cricetus cr				

Db	17 GSCKCKE--CKKCTS-CKKSCCPMG-CAQGCVCK 51	AC Q98S15; DT 01-JUN-2001 ("TREMBLrel. 17, Created) DT 01-JUN-2001 ("TREMBLrel. 17, Last sequence update) DT 01-MAR-2002 ("TREMBLrel. 20, Last annotation update)
RESULT 10		
Q8TEG6	PRELIMINARY;	PRT; 61 AA.
ID Q8TEG6;		
AC Q8TEG6;		
DT 01-JUN-2002 ("TREMBLrel. 21, Created)		
DT 01-JUN-2002 ("TREMBLrel. 21, Last sequence update)		
DT 01-JUN-2002 ("TREMBLrel. 21, Last annotation update)		
DE zinc-induced metallothionein 2A/1A hybrid.		
OS Homo sapiens (Human).		
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
NCBI_TAXID=9606;		
OX NCBI_TAXID=9606;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA Van Weyenberg J., De Ley M.;		
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
DR EMBL; AY07636; AAL76084.1;		
SQ SEQUENCE 61 AA; 6118 MW; 600A7E1F999EFA09 CRC64;		
Query Match	15 0%	Score 58.5; DB 4; Length 61;
Best Local Similarity	35.0%	Pred. No. 2.2;
Matches	14; Conservative	6; Mismatches 15; Indels 5; Gaps 4;
Qy 10 GKCPNEIFSRCDGRQCRCFNPVVKPLCIKICAPGCVCR 49		
Db 17 GSCKCKE--CKKCTS-CKKSCCPMS-CAQGICK 51		
RESULT 11		
Q8UVY1	PRELIMINARY;	PRT; 60 AA.
ID Q8UVY1;		
AC Q8UVY1;		
DT 01-MAR-2002 ("TREMBLrel. 20, Created)		
DT 01-MAR-2002 ("TREMBLrel. 20, Last sequence update)		
DE Metallothionein.		
OS Lithognathus mormyrus (Striped seahream),		
OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi; Neoteleostei;		
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidei;		
OC Sparidae; Lithognathus.		
NCBI_TAXID=50593;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC TISSUE-LIVER;		
RA Tom M.;		
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.		
DR EMBL; AF321007; AAL37187.1;		
DR InterPro; IPR00019; Metallothionein.		
DR InterPro; IPR00006; Metallothionein-vert.		
DR Pfam; PF00131; metallothio. 1.		
DR PRINTS; PRO0060; METALLOTHIONEIN_VRT.		
DR PROSITE; PS00203; METALLOTHIONEIN_VRT.		
SQ SEQUENCE 60 AA; 5936 MW; 78724146693B91B CRC64;		
Query Match	14.8%	Score 58; DB 13; Length 60;
Best Local Similarity	33.3%	Pred. No. 2.5;
Matches	18; Conservative	2; Mismatches 20; Indels 14; Gaps 3;
Qy 7 GGRRKCPNSNEIFSRCDGRQCRCFNPVVKPLCIKICAPGCVCRGLYLRNKKVVC 60		
Db 15 GSCKSC-TNCSCSCKKSCLCCPAGCSK----CASGCCV----KGKTC 54		
RESULT 12		
Q98S15	~ PRELIMINARY;	PRT; 49 AA.
ID Q98S15		

Q8TDC4 PRELIMINARY; PRT; 61 AA.
 ID Q8TDC4;
 AC Q8TDC4;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Metallothionein 1Y.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van Weyenberg J., De Ley M.;
 RT "Identification of molecular targets for zinc regulation of human
 monocyte metabolism";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AF479613; AAL5413.1; -;
 SQ SEQUENCE 61 AA; 6179 MW; 705F96E86B99D1CE CRC64;
 Query Match 13.9%; Score 54.5%; DB 4; Length 61;
 Best Local Similarity 38.5%; Pred. No. 7.5;
 Matches 15; Conservative 4; Mismatches 15; Indels 5; Gaps 4;
 Qy 10 GRCPNSBEIFSRCDGRCQRFCPNVVPKPLC1KICAPGCVYC 48
 Db 17 GSCKCKE-**-**CKCTS-CKKSECCSCCPVG-CAK-CAHGCYC 50
 GN XMRK.
 OS Xiphophorus maculatus (Southern platyfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopercygii; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 NCBI_TAXID=8083;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SR;
 RX MEDLINE=90126443; PubMed=9927468;
 RA Gutbrod H., Schartl M.;
 RT "Intragenic sex-chromosomal crossovers of Xmrk oncogene alleles affect
 RT pigment pattern formation and the severity of melanoma in
 RT Xiphophorus."
 RL Genetics 151:773-783(1999).
 DR EMBL; AF092693; AA003714.1; -;
 DR InterPro: IPR002174; Furin-like.
 DR Pfam; PF00757; Furin-like; 1.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SO SEQUENCE 39 AA; 4195 MW; 42303BA05F6DB557 CRC64;
 Query Match 13.6%; Score 53; DB 13; Length 39;
 Best Local Similarity 42.9%; Pred. No. 7.7;
 Matches 12; Conservative 3; Mismatches 9; Indels 4; Gaps 2;
 Qy 21 CDGRQCREFPNVVPKPL-**-**CIKICAPGC 46
 Db 5 CAEQQNRRORG - PKPIDCCNHEHCAGGC 30



XX Example 2; Page 26; 32pp; English.

PS The present sequence represents a nematode extracted anticoagulant protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The method comprises screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating the prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity; The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

XX Sequence 67 AA;

XX Query Match 100.0%; Score 391; DB 23; Length 67;

XX Best Local Similarity 100.0%; Pred. No. 8e-32;

XX Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 61 AA;

XX Query Match 21.0%; Score 82; DB 20; Length 61;

XX Best Local Similarity 30.9%; Pred. No. 0.37;

XX Matches 17; Conservative 9; Mismatches 19; Indels 10; Gaps 2;

XX Qy 1 CPSNEIFSRCDGRQCRCFNPVVKPLCIKICAPGVCRIGYLRNKKVC 61

XX Db 1 GFGGLGGRKCPNSNEIFSRCDGRQCRCFNPVVKPLCIKICAPGVCRIGYLRNKKVC 60

XX Qy 61 VPRSKCG 67

XX Db 61 VPRSKCG 67

RESULT 3

ID AAB15319 standard; Protein: 61 AA.

XX AAB15319;

AC AC

XX DT 19-DEC-2000 (first entry)

DE N. americanum nematode-extracted anticoagulant protein NamNAP.

XX DE Mature nematode extracted anticoagulant protein; NamNAP; blood clotting;

XX KW Nematode-extracted anticoagulant protein; NamNAP; blood clotting;

XX KW canine hookworm; thrombosis; vaccine.

XX OS Necator americanus.

XX PN US6087487-A.

XX PD 11-JUL-2000.

XX PF 12-FEB-1999; 99US-0249451.

XX PR 17-OCT-1995; 95WO-US13221.

XX PR 17-APR-1997; 97US-0809455.

XX PR 18-OCT-1994; 94US-0326110.

XX PR 05-JUN-1995; 95US-0461995.

XX PR 05-JUN-1995; 95US-0465380.

XX PR 05-JUN-1995; 95US-0486397.

XX PR 05-JUN-1995; 95US-0486399.

XX PR 05-JUN-1995; 95US-0486399.

XX PA (CORV-) CORVAS INT INC.

XX PA Lawvereys MJ, Stanssens PEH, Jespers LS, Gansemans YGJ, Moyle M;

PI Bergum PW, Messens JHL, LaRoche YR, Vlasuk GP;

PI DR 2000-531359/48.

XX DR N-PSDB; AAA73383.

XX PT New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders,

PT comprises nematode-extracted anticoagulant protein domains -

PS Disclosure; Fig 16; 197pp; English.

The present sequence is the *Necator americanus* nematode-extracted anticoagulant protein NamAP. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The protein can also be used as a vaccine against nematode parasites.

for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

Sequence	61 AA:	Sequence	56 AA:
Query Match	21.0%	Score 82;	DB 21;
Best Local Similarity	30.9%	Length 61;	Length 58;
Matches 17; Conservative	9; Mismatches 19;	Pred. No. 0.37;	Best Local Similarity 25.5%;
	Indels 10;	Indels 34;	Matches 14;
	Gaps 2;	Indels 0;	Gaps
Qy .	12 CPSNEIFSRCDGRQCOREPCKVAPKCLIKICAPGCV-----CRIGYLRNKKVVCY 61	Query Match 17.4%;	Score 68;
Db	1 CPSNEIFSRCDGRQCOREPCKVAPKCLIKICAPGCV-----CRIGYLRNKKVVCY 52	Best Local Similarity 25.5%;	DB 20;
	2 CGPNEEYTETGTPCEPKCNEPMPTCTLNIVNCQCKPGFKGPKGCVAPGPGC 57	Matches 14;	Length 58;

RESULT 4	AAY30433	Mature nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; Factor VIIa/TF.
	AAY30433	Nematode extracted anticoagulant protein; NAP.
15-NOV-1999	(first entry)	
		Helimicrocosmidae colvourus
RESULT 5	AAY57812	
	ID AAY57812	standard; protein; 59 AA.
	XX	
	AC AAY57812;	
	XX	
	DT 22-MAR-2000	(first entry)
	XX	
	DE	Trout metallothionein Class I amino acid sequence.
	XX	
	KW	Metallothionein; metal recovery; remediation; heavy metal;
	KW	precious metal; phytochelatin; green algae; Chlamydomonas reinhardtii.
	XX	
	OS	Salmo sp.
	VV	

Disclosure: Column 3; 9pp; English.

The present sequence represents mammalian metallothionein. It is used to produce chimeric proteins of the invention. The specification describes a recombinant bifunctional streptavidin-metallothionein chimeric protein. This protein is produced by introducing into a host cell nucleic acid encoding a bifunctional fusion protein having a streptavidin and a metallothionein moiety, and incubating the cell to express the fusion protein. The streptavidin moiety consists of residues 16-133 of mature streptavidin. The chimeric protein is used to incorporate heavy metal ions into biological materials containing biotin, or to remove heavy metal ions from the biological material. Specific uses include loading cancerous tissue with heavy metal ions for imaging of tumour cells and radiotherapy, and labelling DNA and proteins for detection on gels or blots by surface scanning mass spectrometry.

WO200222821-A2.
21-MAR-2002.
13-SEP-2001; 2001WO-US28429.
13-SEP-2000; 2000US-323569P.
11-SEP-2001; 2001US-0950933.
(PION-) PIONEER HI-BRED INT INC.
Simmons CR, Navarro Acevedo PA;
WPI; 2002-425842/45.

Disclosure: Page 154; 163pp; English.

The invention relates to an isolated polynucleotide encoding a polypeptide which is related to potato snakin antimicrobial protein and GASA4 or GASA5 or GAST homologues, which is referred to as lysine- and cysteine-rich peptides (KCP)-like polypeptide, having a nucleotide sequence from 36 recombinant expression cassette comprising the isolated polynucleotide of the invention is useful for modulating the level of (KCP)-like polypeptides in a plant cell, where the level of (KCP)-like polypeptides is increased and disease resistance is enhanced.

CC anti-coagulants protein C and antithrombin III), human
 CC alpha-1-antitrypsin, PEA-3 protein and reporter proteins such as
 CC luciferase. Preferred promoters for use in such age-regulatable
 CC expression vectors include the human factor IX promoter, the T7 promoter,
 CC the T3 promoter and the SP6 promoter. The expression vectors of the
 CC invention may be used in gene therapy to provide age-related and/or
 CC liver-specific expression of target genes. Age-regulatable constructs may
 CC be used in the treatment of such age-related conditions such as
 CC thrombosis, cardiovascular disease, diabetes, Alzheimer's disease,
 CC Parkinson's disease, cancer, osteoporosis, osteoarthritis and dementia.
 Specifically, they may be used to express factor IX antisense mRNA in the
 CC treatment of thrombotic conditions associated with the natural
 CC age-related rise in factor IX expression. Transgenic cells or animals
 CC that contain vectors of the invention are useful as models of these
 CC diseases in screening for potential therapeutic agents and for studying
 CC normal processes such as ageing and gene expression. Fragments and
 CC homologues of age-related regulatory sequences, are useful as probes to
 CC detect, isolate or identify other such sequences in samples. The present
 CC sequence represents a fragment of HFIX.

XX Sequence 43 AA:

Query	Match	Score 62;	DB 22;	Length 43;
Best Local Matches	Similarity 33.3%;	Pred. No. 26;		
14;	Conservative 5;	Mismatches 15;	Indels 8;	Gaps 2;

XX 22 DGRCQRFCPNNVPKPLCIRKICAPGCVCRIGY-LRNKKVVCVP 62
 Qy 8 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 8 NGRCEQFKCKNSADNRKV-----CSCTEGYRLAENQKSCEP 42

RESULT 10

AAV57822 standard; protein; 61 AA.

XX AAV57822;

XX 22-MAR-2000 (first entry)

DE Rabbit liver metallothionein Class II amino acid sequence.
 XX Metallothionein: metal recovery; remediation; heavy metal;
 KW precious metal; phytoceratin; green algae; Chlamydomonas reinhardtii.
 XX Oryctolagus cuniculus.
 OS WO9960838-A1.
 XX 02-DEC-1999.
 XX 28-MAY-1999; 99WO-US12007.
 PR 28-MAY-1998; 98US-0087374.
 XX (OHIS) UNIV OHIO STATE RES FOUND.
 PI Sayre RT, Traina SJ;
 XX DR; 2000-086645/07.
 PR Novel method for metal recovery, remediation and separation -
 XX Disclosure: Fig 1; 86pp; English.
 PS

XX The present invention describes a transgenic algal cell (1) of the
 CC genus Chlamydomonas comprising a recombinant genetic material comprising
 CC a nucleotide sequence capable of expressing chicken type I
 CC Metallothionein. Also described is a method of removing metal from
 CC an aqueous medium containing at least one dissolved or suspended
 CC metal. The transgenic algae are used for the selective separation of
 CC metals, particularly the separation of precious and desirable metals
 CC such as gold and uranium, from other metals such as cadmium, zinc and
 CC copper. The method can be used to facilitate the selective recovery of
 CC

CC precious and rare metals from mineral sources where aqueous media can
 CC be used, such as in natural source water flows, ground water and where
 CC water may be introduced. The method is suitable for well-drilling,
 CC soil and water remediation arts, mining fields, and industrial
 CC engineering. The present sequence represents a Class II metallothionein
 CC given in the present invention.

XX Sequence 61 AA:

Query	Match	Score 62;	DB 21;	Length 61;
Best Local Matches	Similarity 38.5%;	Pred. No. 36;		
15;	Conservative 2;	Mismatches 10;	Indels 12;	Gaps 3;

XX 11 KCPSENEIFSRCDQRCPNVPKPLCIKTCAPGVYCR 49
 Qy 25 KCTTS-----CRKSCSCSCP-----PGCAK-CAQGCTCK 51
 Db 25

RESULT 11
 ID AAB61455
 ID AAB61455 standard; protein; 67 AA.
 XX
 AC AAB61455;
 XX
 DT 04-APR-2001 (first entry)
 XX Metallothionein domain consensus.
 DE
 XX TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung;
 KW autoimmune; allergy; cardiovascular; brain; degenerative; placental;
 KW pancreatic; skeletal; muscle.
 XX
 OS Synthetic.
 XX
 PN WO200100672-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-US18184.
 XX
 PR 29-JUN-1999; 99US-0342687.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Holtzman DA, Barnes TM, Fraser CC, Sharp JD;
 XX
 DR WPI; 2001-050127/06.
 XX
 PT Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and
 MANGO 245 proteins, useful in the treatment of inflammatory diseases
 (e.g., idiopathic ulcerative colitis), tumors, renal disorders and liver
 disorders (e.g., jaundice) -
 XX
 PS Disclosure: Fig 13; 262pp; English.
 XX
 CC The present invention relates to cDNAs encoding TANGO 244,
 CC TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.
 CC The nucleic acids, proteins and protein modulators are useful for
 CC treating colonic disorders, inflammatory diseases, tumors,
 CC renal disorders, liver disorders, lung disorders, autoimmune diseases,
 CC allergic diseases, cardiovascular diseases, brain disorders,
 CC degenerative diseases, pancreatic, skeletal and muscle
 CC disorders.
 XX
 SQ Sequence 67 AA;

Query	Match	Score 61.5%;	DB 22;	Length 67;
Best Local Matches	Similarity 31.7%;	Pred. No. 43;		
19;	Conservative 5;	Mismatches 29;	Indels 7;	Gaps 2;

Qy 1 GGFGGLGGRKGPSPNEIIIFSRCDQRCPNVPKPLCIKTCAPGVYCR 60
 Db 11 GGSGCTGTGCKNCCTS-CRKSCSCSCPAGSK-----CAGGCVKGGGAASETSKC 63

RESULT 12
 AAY04648 standard; peptide: 47 AA.
 ID XX
 AC AAY04648;
 XX DT 22-JUN-1999 (first entry)
 XX DE Factor IXa catalytic and interacting domains.
 XX KW Receptor; catalytic domain; Factor IXa; tissue factor; angina;
 blood clotting disorder; thrombosis; restenosis; myocardial infarction;
 reclosure; cerebrovascular disease; hypercoagulability; anticoagulant;
 peripheral arterial occlusive disease; pulmonary embolism; cyclic.
 XX OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Disulfide-bond 8..19
 FT Domain 10..12 /note= "Factor VIIIa interacting domain"
 FT Disulfide-bond 13..29
 FT Domain 14..16 /note= "catalytic domain"
 FT Disulfide-bond 31..44
 XX PN WO9113062-A1.
 XX PD 18-MAR-1999.
 XX PF 08-SEP-1998; 9BWO-GB02700.
 PR 09-SEP-1997; 97GB-0019157.
 XX PA (MATTWNS D P.
 PA (NYCOMED IMAGING AS.
 XX PI Fischer PM, Sakariassen KS,
 XX DR WPI; 1999-215061/18.
 XX PT New anticoagulant compounds
 PS Disclosure: Fig 1; 50pp; English.
 XX CC Peptides AAY04625-Y04647 represent claimed compounds which are capable
 of interacting with an internal receptor in the catalytic domain of
 Factor IXa (FXa) or Factor X (FX) defined by the residues Ile290,
 CC Asp291, Tyr292, Thr293, Glu294, Glu374 and Phe378 of FXa, and Leu300,
 Pro301, Glu302, Trp305, Ala306, Lys385 and Phe389 of FXa, or the ligand
 CC defined by residues Cys95-Cys99 of FXa or Cys96-Cys100 of FXa. The
 CC compounds can be used to prevent the formation of a functional
 CC FVIIa/FIXa or FVIIIa/FXa complex, so can be used to combat or prevent
 CC blood clotting disorders, e.g. thrombosis (particularly vascular
 CC thrombosis or deep vein thrombosis), acute myocardial infarction,
 CC arterial occlusive disease, cerebrovascular disease, peripheral
 CC arterial occlusive disease, hypercoagulability or pulmonary embolism.
 CC They can also be used to prevent the occurrence of blood clotting
 CC disorders caused by e.g. grafting surgery, vessel wall potency
 CC restoration or sepsis.
 XX SQ Sequence 47 AA;

RESULT 13
 AAB44778 standard; Protein: 56 AA.
 ID XX
 AC AAB44778;
 XX DT 12-FEB-2001 (first entry)
 XX DE Human secreted protein sequence encoded by gene 17 SEQ ID NO:77.
 XX KW antirheumatic; antiproliferative; nootropic; neuroprotective; antibacterial;
 cerebroprotective; cytostatic; cardiotonic; virucide;
 fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
 hyperproliferative disorder; cardiovascular disorder; angiogenesis;
 cerebrovascular disorder; nervous system disorder; ocular disorder;
 wound healing; skin aging; food additive; preservative.

Claim 11: Page 362; 391pp; English.

The polynucleotide sequences given in AAC79799 to AAC79848 encode the human secreted proteins given in AAB44762 to AAB44811. AAB44812 to AAB4429 represent human secreted polypeptide sequences and proteins homologous to them, which are used in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells in the genes are expressed in. Examples of activities are: immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiotonic; vasotropic; nootropic; neuroprotective; antibacterial; fungicide; and ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, cerebrovascular disorders, angiogenesis, nervous system disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities AAC79790 to AAC79798 and AAB44761 represent sequences used in the exemplification of the present invention.

Query Match 15.6%; Score 61; DB 20; Length 47;
Best Local Similarity 34.1%; Pred. No. 36;
Matches 14; Conservative 4; Mismatches 15; Indels 8; Gaps 2;

Query 23 GRCCREFCPNVPKPKLICIKAPGCVRLIGY-LRNKKKVCP 62
 111:111 : 1 | 1 | 1 : 1 |
Db 13 GRCEQFCCKNSADNKVV-----CSCTEGYRLAENQKSCCP 46

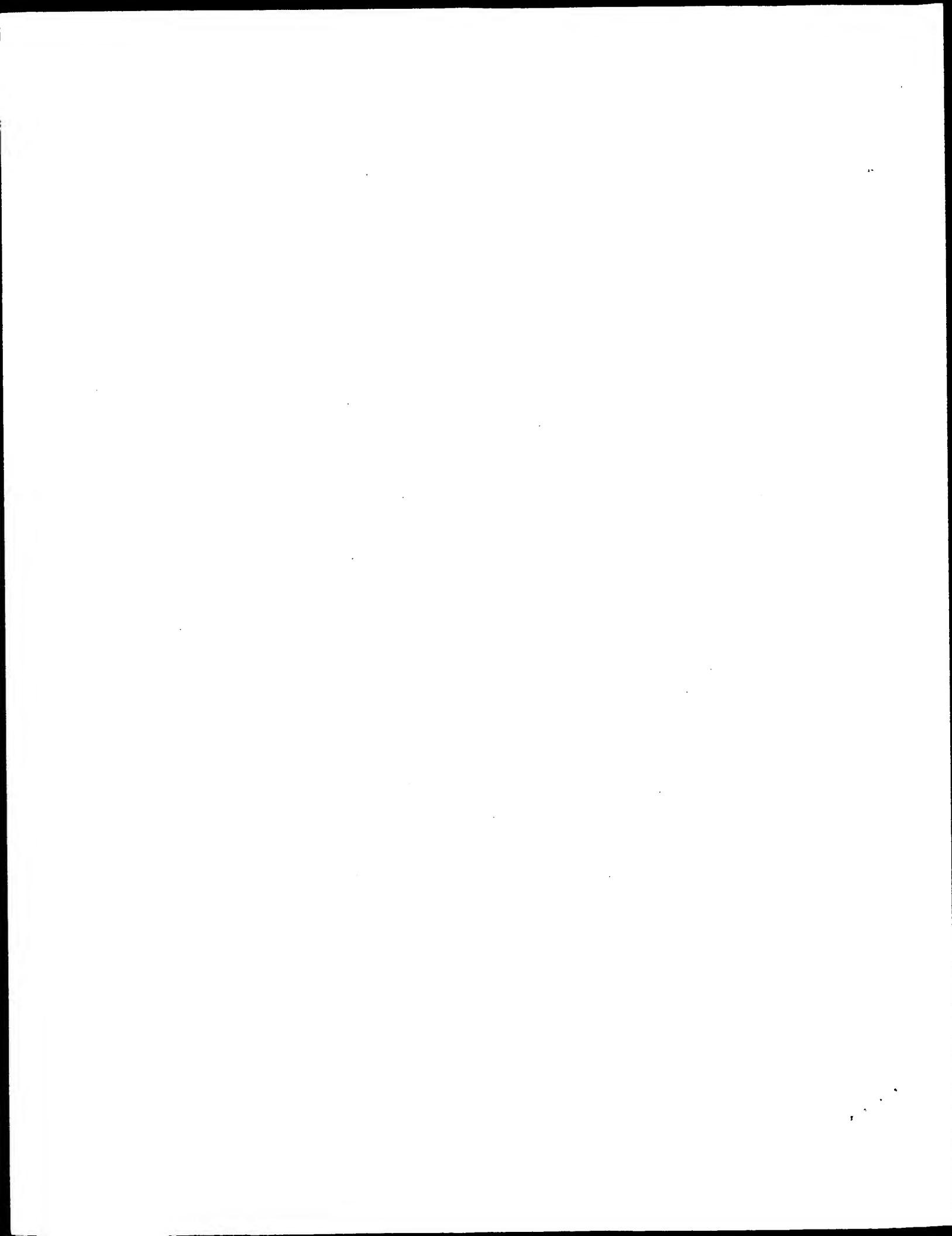
Sequence 56 AA;
Query Match 15.6%; Score 61; DB 21; Length 56;
Best Local Similarity 29.8%; Pred. No. 42;

protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <http://wipo.int/nub/unpublished> not sequences

Sequence Alignment Results for Protein Sequences						
XX	SQ	Sequence	60 AA:			
		Query Match	15.3%	Score 60;	DB 23;	Length 60;
		Best Local Similarity	35.5%	pred. No.	56;	
		Matches / 11; Conservative	3;	Mismatches	17;	Indels 0;
						Gaps 0;
QY	36	PLCIKICAPGCVCRGLYRLNKKVCPRSKC	66			

Search completed: February 26, 2003, 15:10:41



Result No.	Score	Match Length	DB ID	Description
1	63	16	1	Sequence 59, Appl
2	62.5	16	0	Sequence 76, Appl
3	57.5	14	7	Sequence 115, Appl
4	56.5	14	5	Sequence 120, Appl
5	55.5	14	2	Sequence 47, Appl
6	55.5	14	2	Sequence 11, Appl
7	55.5	14	2	Sequence 11, Appl
8	55.5	14	2	Sequence 11, Appl
9	55.5	14	2	Sequence 11, Appl
10	55.5	14	2	Sequence 12, Appl
11	54.5	13	9	Sequence 11, Appl
12	53	13	6	Sequence 11, Appl
13	49	12	5	Sequence 73, Appl
14	49	12	5	Sequence 173, Ap
15	49	12	5	Sequence 1792, Ap
16	49	12	5	Sequence 2056, Ap
17	48.5	12	4	Sequence 3762, A
18	48.5	12	4	Sequence 2, Appli
19	48.5	12	4	Sequence 8, Appli

Db 17 GCKPKNP--PRSIGTCVELGQDQSCPNTORCCSNGCGHVKC 56

RESULT 2
US-09-950-933A-76
; Sequence 76, Application US/09950933A

; Patent No. US2002016614A1

; GENERAL INFORMATION:

; APPLICANT: Simmons, Carl R.

; APPLICANT: Navarro, Pedro

; TITLE OF INVENTION: Antimicrobial Peptides and Methods of

; TITLE OF INVENTION: Use

; FILE REFERENCE: 35718/238472

; CURRENT APPLICATION NUMBER: US/09/950,933A

; CURRENT FILING DATE: 2001-09-11

; PRIORITY NUMBER: 66/232,569

; PRIOR FILING DATE: 2000-09-13

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 76

; LENGTH: 63

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

Query Match 16.0%; Score 62.5; DB 9; Length 63;

Best Local Similarity 37.8%; Pred. No. 8.9;

Matches 17; Conservative 4; Mismatches 19; Indels 5; Gaps 3;

; GENERAL INFORMATION:

; APPLICANT: Lasek, Amy W.

; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER

; FILE REFERENCE: PA-0038 US

; CURRENT APPLICATION NUMBER: US/09/981,353

; CURRENT FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 194

; SOFTWARE: PERL Program

; SEQ ID NO: 115

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20020160382A1 26856766CD1

Query Match 14.7%; Score 57.5; DB 9; Length 61;

Best Local Similarity 32.8%; Pred. No. 26;

Matches 15; Conservative 6; Mismatches 20; Indels 5; Gaps 4;

; GENERAL INFORMATION:

; APPLICANT: Jones, David A.

; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER

; FILE REFERENCE: PA-0038 US

; CURRENT APPLICATION NUMBER: US/09/981,353

; CURRENT FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 194

; SOFTWARE: PERL Program

; SEQ ID NO: 115

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US/09/981,353

Query Match 14.2%; Score 55.5; DB 10; Length 38;

; Sequence 120, Application US/09981353

; Patent No. US20020160382A1

; GENERAL INFORMATION:

; APPLICANT: Lasek, Amy W.

; APPLICANT: Jones, David A.

; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER

; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353

; CURRENT FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 194

; SOFTWARE: PERL Program

; SEQ ID NO: 120

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20020160382A1 2757583CD1

US-09-981-353-120

; LENGTH: 61;

; Query Match 14.5%; Score 56.5; DB 9; Length 61;

; Best Local Similarity 37.5%; Pred. No. 33;

; Matches 15; Conservative 5; Mismatches 15; Indels 5; Gaps 4;

; Qy 10 GKCPSENEFSRCDGRCORECPNVPKPLCIKICAPGCVC 49

; Db 17 GSCRCKE--CKCCTS-CKSCCSCCPVG-CSK-CAQGCCK 51

RESULT 5
US-09-847-185-47

; Sequence 47, Application US/09847185

; Patent No. US20020076592A1

; GENERAL INFORMATION:

; APPLICANT: SOO HOO, William

; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS

; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE

; RESPONSE USING SAME

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL & FLORES, LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/847,185

; FILING DATE: 01-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/201,931

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IM 2442

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)535-9001

; TELEFAX: (619)535-8949

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; TOPOLOGY: Linear

; MOLECULE TYPE: Peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 47:

; US-09-847-185-47

; Sequence 4, Application US/09981353

; Patent No. US20020160382A1

; GENERAL INFORMATION:

; APPLICANT: Lasek, Amy W.

; APPLICANT: Jones, David A.

; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER

; FILE REFERENCE: PA-0038 US

; CURRENT APPLICATION NUMBER: US/09/981,353

; CURRENT FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 194

; SOFTWARE: PERL Program

; SEQ ID NO: 120

; LENGTH: 61;

; Query Match 14.2%; Score 55.5; DB 10; Length 38;

; Best Local Similarity 29.8%; Pred. No. 27;

; Matches 14; Conservative 0; Mismatches 14; Indels 19; Gaps 2;

; Qy 2 GFGGLGGRKCPSENEFSRCDGRCORECPNVPKPLCIKICAPGCVC 48

; Db 11 GSCACAGSCKE--CKCTS-CKSCCSCCPVG-CSK-CAQCCICK 51

Db 1 GCGAGGGGCC-----CTAGC-----ACCCACCCGGCT 28
RESULT 6
 US-10-136-573A-11
 ; Sequence 11, Application US/10136573A
 ; GENERAL INFORMATION:
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Mark, Melanie Rose
 ; APPLICANT: Zhang, Dong Xiao
 ; TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related Ligands and
 ; FILE REFERENCE: P1084R1C2
 ; CURRENT FILING DATE: 2002-04-29
 ; PRIOR APPLICATION NUMBER: US 09/480,977
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: US 08/899,437
 ; PRIOR FILING DATE: 1997-07-24
 ; PRIOR FILING DATE: 1997-07-09
 ; NUMBER OF SEQ ID NOS: 23
 ; SEQ ID NO 11
 ; LENGTH: 45
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-136-573A-11

Query Match 14.2%; Score 55.5%; DB 9; Length 45;
 Best Local Similarity 35.9%; Pred. No. 31;
 Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 2;
 Qy 1B FSRCDGRCQRFCPNPVKPLCIKICA---PGCVCRIGYL 53
 Db 2 FSRCPKQYKHYC---IKGRCRFVVAEQTPSCVCDGYI 36

RESULT 7
 US-09-877-665-11
 ; Sequence 11, Application US/09877665
 ; Patent No. US2002164680A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
 ; TITLE OF INVENTION: Erbb Receptor Specific Neuregulin Related Ligands and
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpartin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/877,665
 FILING DATE: 08-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/109,206
 FILING DATE: 30-Jun-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Conley, Deirdre L.
 REGISTRATION NUMBER: 36,487
 REFERENCE/DOCKET NUMBER: P1084R1-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-2066

; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; FEATURE:
 ; NAME/KEY: hbRC.efg
 ; LOCATION: 1-45
 ; IDENTIFICATION METHOD:
 ; OTHER INFORMATION:
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 ;
 ; Query Match 14.2%; Score 55.5%; DB 9; Length 45;
 ; Best Local Similarity 35.9%; Pred. No. 31;
 ; Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 2;
 Qy 1B FSRCDGRCQRFCPNPVKPLCIKICA---PGCVCRIGYL 53
 Db 2 FSRCPKQYKHYC---IKGRCRFVVAEQTPSCVCDGYI 36
RESULT 8
 US-10-215-862-11
 ; Sequence 11, Application US/10215862
 ; Publication No. US2003016166A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Mark, Melanie Rose
 ; APPLICANT: Zhang, Dong Xiao
 ; TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related Ligands and
 ; FILE REFERENCE: P1084R1D2C1
 ; CURRENT APPLICATION NUMBER: US/10/215,862
 ; CURRENT FILING DATE: 2002-09-24
 ; PRIOR APPLICATION NUMBER: US 09/126,663
 ; PRIOR FILING DATE: 1998-07-30
 ; PRIOR APPLICATION NUMBER: US 08/899,437
 ; PRIOR FILING DATE: 1997-07-24
 ; PRIOR APPLICATION NUMBER: US 09/052,019
 ; PRIOR FILING DATE: 1997-07-09
 ; NUMBER OF SEQ ID NOS: 23
 ; SEQ ID NO 11
 ; LENGTH: 45
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-215-862-11

Query Match 14.2%; Score 55.5%; DB 9; Length 45;
 Best Local Similarity 35.9%; Pred. No. 31;
 Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 2;
 Qy 1B FSRCDGRCQRFCPNPVKPLCIKICA---PGCVCRIGYL 53
 Db 2 FSRCPKQYKHYC---IKGRCRFVVAEQTPSCVCDGYI 36
RESULT 9
 US-09-817-647-11
 ; Sequence 11, Application US/09817647
 ; Patent No. US2002008222A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
 ; TITLE OF INVENTION: Erbb Receptor-Specific Neuregulin Related Ligands and Uses Therefor
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/817,647
 FILING DATE: 26-Mar-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 FILING DATE: 09/107,979
 ATTORNEY/AGENT INFORMATION:
 NAME: Conley, Deirdre L.
 REFERENCE/DOCKET NUMBER: 36,487
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/932-2066
 TELEFAX: 650/932-9881
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 FEATURES:
 NAME/KEY: hBTC_efg
 LOCATION: 1-45
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-817-647-11

Query Match 14.2%; Score 55.5%; DB 9; Length 46;
 Best Local Similarity 35.9%; Pred. No. 32;
 Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 2;

Qy 18 FSRCDGRCQRCPNVPKPLIKICA--PGCVRLGYL 53
 Db 2 FSRCPKQYKHC---IKGRCRFVVAEQTPSCVCDEGYI 37

RESULT 11
 US-09-865-578-11
 Sequence 11, Application US/09865578
 Patent No. US2001003443A1

GENERAL INFORMATION:
 APPLICANT: E. MARTIN, SPENCER
 TITLE OF INVENTION: HUMAN SOMATOMEDIAN CARRIER PROTEIN SUBUNITS
 AND PROCESS FOR PRODUCING THEM; RECOMBINANT DNA MOLECULES,
 HOSTS, PROCESSES AND HUMAN SOMATOMEDIAN CARRIER PROTEIN-LIKE
 PROTEINS
 FILE REFERENCE: 057491/0680
 CURRENT APPLICATION NUMBER: US/09/865,578
 PRIOR APPLICATION NUMBER: 09/397,192
 PRIOR FILING DATE: 2001-05-29
 PRIOR APPLICATION NUMBER: 09/162,118
 PRIOR FILING DATE: 1999-09-16
 PRIOR APPLICATION NUMBER: 09/397,192
 PRIOR FILING DATE: 1999-09-03
 PRIOR APPLICATION NUMBER: 08/706,755
 PRIOR FILING DATE: 1996-09-03
 PRIOR APPLICATION NUMBER: 08/437,407
 PRIOR FILING DATE: 1995-05-12
 PRIOR APPLICATION NUMBER: 08/320,123
 PRIOR FILING DATE: 1994-10-07
 PRIOR APPLICATION NUMBER: 08/043,039
 PRIOR FILING DATE: 1993-04-05
 PRIOR APPLICATION NUMBER: 07/763,481
 PRIOR FILING DATE: 1991-09-20
 PRIOR APPLICATION NUMBER: 07/290,250
 PRIOR FILING DATE: 1988-12-22
 PRIOR APPLICATION NUMBER: 07/170,022
 SEQ ID NO: 11
 LENGTH: 58
 TYPE: PRT
 ORGANISM: Homo Sapiens

Query Match 13.9%; Score 54.5%; DB 10; Length 58;
 Best Local Similarity 34.6%; Pred. No. 49;

Matches 18; Conservative 2; Mismatches 15; Indels 17; Gaps 4; Other information: EXPRESSED IN LUNG, SIGNAL = 0.89
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
 US-09-864-761-34955

Query Match 13 6%; Score 53; DB 10; Length 46;
 Best Local Similarity 48.1%; Pred. No. 55; Mismatches 5; Indels 8; Gaps 1;

Y 1 GGFGGGKCPNSMEFSPRCGCRQR 27
 Db 10 GGAGGGGRCKTR-----DGRIRR 28

RESULT 12
 US-09-854-761-34955
 Sequence 34995 Application US/09864761
 Patent No. US200420048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MICROARRAY
 FILE REFERENCE: Ascomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006663
 PRIOR FILING DATE: 2001-01-30
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2001-01-29
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 34995
 LENGTH: 46
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AB020862.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
 OTHER INFORMATION: EXPRESSED IN BT74, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
 OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.7
 OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 2.2

RESULT 13
 US-09-917-340-73
 Sequence 73 Application US/09917340
 Parent No. US20020090369A1
 GENERAL INFORMATION:
 APPLICANT: Murphy, Christopher J.
 APPLICANT: McAnulty, Jonathan F.
 APPLICANT: Reid, Ted W.
 TITLE OF INVENTION: Transplant Media
 FILE REFERENCE: TPLANT-06168
 CURRENT APPLICATION NUMBER: US/09/917,340
 CURRENT FILING DATE: 2001-07-29
 PRIOR APPLICATION NUMBER: 60/221,632
 PRIOR FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: 60/249,602
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/290,932
 PRIOR FILING DATE: 2001-05-15
 NUMBER OF SEQ ID NOS: 96
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 73
 LENGTH: 40
 TYPE: PRT
 ORGANISM: Aedes aegypti
 US-09-917-340-73

Query Match 12 5%; Score 49; DB 10; Length 40;
 Best Local Similarity 48.0%; Pred. No. 1.2e+02; Mismatches 2; Indels 9; Gaps 1;

Y 42 CAPGCVCR -LGVLRLNKKVCPVRS 64
 Db 16 CAAHClARGNRGSGCNSKVKCVCRN 40

RESULT 14
 US-09-796-692-11773
 Sequence 1173 Application US/09796692
 Publication No. US20020198362A1
 GENERAL INFORMATION:
 APPLICANT: Gaiger, Alexander
 APPLICANT: Algate, Paul A.
 APPLICANT: Mannion, Jane
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES
 FILE REFERENCE: 2077.001200
 CURRENT APPLICATION NUMBER: US/09/7796,692
 CURRENT FILING DATE: 2001-03-01
 PRIOR APPLICATION NUMBER: 60/186,126
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: 60/190,479
 PRIOR FILING DATE: 2000-03-17
 PRIOR APPLICATION NUMBER: 60/200,545
 PRIOR FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: 60/200,303
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/200,779
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/200,999
 PRIOR FILING DATE: 2000-05-01

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; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 1773
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-692-1773

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Query Match 12.5%; Score 49; DB 9; Length 54;
Best Local Similarity 30.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 3; Mismatches 22; Indels 14; Gaps 3;
Qy 8 GRGKCP-----SNEIFSRCDGRCORFCPNNVPKPLKIKICAPGCCVRLG 51
Db 2 QELCPVPAATISTHVHSSLRPRPGCIPG-LPHPTSIRSC-PRMSSLG 49

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RESULT 15

US-09-796-692-1792
; Sequence 1792, Application US/09796692
; Publication No. US20020198362A1

GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY

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; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077_00100
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 1792
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-692-1792

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Query Match 12.5%; Score 49; DB 9; Length 64;
Best Local Similarity 30.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 3; Mismatches 22; Indels 14; Gaps 3;
Qy 4 GGIGGRGCPNSNEIFSRCDGRC----QRFCPNVVPKPL---CIRKCAPGCCVRLG 51
Db 4 GGARRAPCRS-----CATRCWGSTHSRWCYSTEPPSPVPCRSQTSGCWLRG 53

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;

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: February 26, 2003, 15:10:48 ; Search time 352 Seconds
(without alignments)
122,719 Million cell updates/sec

Title: US-09-506-978-1
Perfect score: 391
Sequence: 1 GGFGGLGGRGKCPSENFSR.....CRLGYLRNKKVCPRSRGCG 67

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 27591442

Minimum DB seq length: 0
Maximum DB seq length: 67

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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 3: /cgn2_6/podata/1/paa/US07_COMB.pep:*
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 26: /cgn2_6/podata/1/paa/US102_COMB.pep:*
 27: /cgn2_6/podata/1/paa/US106_COMB.pep:*

RESULT 1
US-09-506-978-1
; Sequence 1, Application US/09506978
; GENERAL INFORMATION:
; APPLICANT: Spertini, Francois
; TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 18519-001
; CURRENT APPLICATION NUMBER: US/09-506-978
; CURRENT FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Apis mellifera
US-09-506-978-1

ALIGNMENTS

Query Match 100.0%; Score 391; DB 19; Length 67;
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

Result No.	Score	Query Match	Length	DB ID	Description
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2	391	100.0	67	25	US-10-174-151-1
3	391	100.0	67	26	US-10-204-145-1
4	113.5	29.0	62	27	US-60-142-896-1491
5	113.5	29.0	62	27	US-60-145-138-701
6	88.5	22.6	62	21	US-09-791-537-9664

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db 1 GOERCGPNEVWTECTG-CEMKGDENTPCPLMCR - RPSCECSPGRGMRTNDGRC1PA 7 ; CURRENT FILING DATE: 1999-10-29
 Qy 64 SKC 66 ; NUMBER OF SEQ ID NOS: 5442
 Db 58 SQC 60 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3339
 ; LENGTH: 54
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-60-162-247-3339

RESULT 7
 ; Sequence 3377, Application US/60160203-3377
 ; GENERAL INFORMATION:
 ; APPLICANT: BONAZZI, VIVIEN
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS AND
 ; TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: CL000116
 ; CURRENT FILING DATE: 1999-10-19
 ; CURRENT APPLICATION NUMBER: US/60/160,203
 ; NUMBER OF SEQ ID NOS: 6374
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3377
 ; LENGTH: 39
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 ; US-60-160-203-3377

Query Match 22.3%; Score 87; DB 27; Length 39;
 Best Local Similarity 34.1%; Pred. No. 0.28; Indels 2; Gaps 1;
 Matches 14; Conservative 7; Mismatches 18;

Qy 11 KCPNSNEIFSRCDGRCORFCPNVPKPLCITIKAPGCVCRGLG 51
 Db 1 QCPANQVYQEGSACVTKCSN - PQHSSSSCTFGCFPEG 39

RESULT 8
 ; Sequence 5102, Application US/60169840
 ; GENERAL INFORMATION:
 ; APPLICANT: Bonazzi, Vivien
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS AND
 ; TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: CL000164
 ; CURRENT FILING DATE: 1999-12-09
 ; CURRENT APPLICATION NUMBER: US/60/169,840
 ; NUMBER OF SEQ ID NOS: 9628
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 5102
 ; LENGTH: 39
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-60-169-840-5102

Query Match 22.3%; Score 87; DB 27; Length 39;
 Best Local Similarity 34.1%; Pred. No. 0.28; Indels 2; Gaps 1;
 Matches 14; Conservative 7; Mismatches 18;

Qy 11 KCPNSNEIFSRCDGRCORFCPNVPKPLCITIKAPGCVCRGLG 51
 Db 1 QCPANQVYQEGSACVTKCSN - PQHSSSSCTFGCFPEG 39

RESULT 9
 ; Sequence 3339, Application US/60162247
 ; GENERAL INFORMATION:
 ; APPLICANT: Bonazzi, Vivien
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS AND
 ; TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: CL000127
 ; CURRENT APPLICATION NUMBER: US/60/162,247

Db 1 QCPFSHYSVCTSSCPDTCSDLTASRNATCPTEGCECNQGFVLSTSQ-CVPLHK 54

RESULT 10
 ; Sequence 1334, Application US/60163123
 ; GENERAL INFORMATION:
 ; APPLICANT: BONAZZI, Vivien
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ; TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: CL000137
 ; CURRENT APPLICATION NUMBER: US/60/163,123
 ; NUMBER OF SEQ ID NOS: 1986
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1354
 ; LENGTH: 53
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-60-163-123-1354

Query Match 21.6%; Score 84.5; DB 27; Length 53;
 Best Local Similarity 30.9%; Pred. No. 0.66; Mismatches 8; Indels 1; Gaps 1;
 Matches 17; Conservative 8;

Qy 11 KCPNSNEIFSRCDGRCORFCPNVPKPLCITIKAPGCVCRGLG 62
 Db 3 QCPFSHYSVCTSSCPDTCSDLTASRNATCPTEGCECNQGFVLSTSQ-CVPLHK 53

RESULT 11
 ; Sequence 1440, Application US/60163123
 ; GENERAL INFORMATION:
 ; APPLICANT: Bonazzi, Vivien
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
 ; TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: CL000137
 ; CURRENT APPLICATION NUMBER: US/60/163,123
 ; NUMBER OF SEQ ID NOS: 1986
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1440
 ; LENGTH: 53
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-60-163-123-1440

Query Match 21.6%; Score 84.5; DB 27; Length 53;
 Best Local Similarity 30.8%; Pred. No. 0.66; Mismatches 8; Indels 1; Gaps 1;
 Matches 16; Conservative 8;

Qy 11 KCPNSNEIFSRCDGRCORFCPNVPKPLCITIKAPGCVCRGLG 62
 Db 3 QCPFSHYSVCTSSCPDTCSDLTASRNATCPTEGCECNQGFVLSTSQ-CVPLHK 53

RESULT 12
US-60-160-203-4-074
Sequence 4074, Application US/60160203
GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000116
CURRENT APPLICATION NUMBER: US/60/160,203
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 6374
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4074
LENGTH: 60
TYPE: PRT
ORGANISM: HUMAN
US-60-160-203-4-074

Query Match 21.5%; Score 84; DB 27; Length 60;
Best Local Similarity 31.7%; Pred. No. 0.83; Mismatches 10; Indels 20; Gaps 4;
Matches 20; Conservative 13; Indels 20; Gaps 4;

Qy 11 KCPSENEIFSRC-----DGRCQRFCPNVVPKPLCIKICAPGCVCRLOGYLRLNKKV 59
Db 7 ECPAYSSYTNCPLSPSCWLDGRCE--GAKVP----SACAEGCICQPGVLSEDK- 57

RBSRESULT 15
US-60-169-840-5359
; Sequence 5359, Application US/60169840
GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000154
CURRENT APPLICATION NUMBER: US/60/169,840
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 9628
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5359
LENGTH: 63
TYPE: PRT
ORGANISM: Human
US-60-169-840-5359

Query Match 21.1%; Score 82.5; DB 27; Length 63;
Best Local Similarity 32.1%; Pred. No. 1.2; Mismatches 8; Indels 1; Gaps 1;
Matches 18; Conservative 13; Indels 29; Gaps 1;

Qy 12 CPSNEIFSRCDCDRCQRFCPNVVPKPLCIKICAPGCVCRLOGYLRLNKKVPRSKG 67
Db 1 CPAHSHYSICTRTCGSCCAALSGLITGCTRCFEGCECDRFLS-QGVCIIPVQDCG 55

Search completed: February 26, 2003, 15:19:21
Job time : 353 secs

RESULT 13
US-60-163-123-1552
Sequence 1552, Application US/60163123
GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000137
CURRENT APPLICATION NUMBER: US/60/163,123
CURRENT FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 1986
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1552
LENGTH: 60
TYPE: PRT
ORGANISM: Human
US-60-163-123-1552

Query Match 21.5%; Score 84; DB 27; Length 60;
Best Local Similarity 31.7%; Pred. No. 0.83; Mismatches 10; Indels 20; Gaps 4;
Matches 20; Conservative 13; Indels 20; Gaps 4;

Qy 11 KCPSENEIFSRC-----DGRCQRFCPNVVPKPLCIKICAPGCVCRLOGYLRLNKKV 59
Db 7 ECPAYSSYTNCPLSPSCWLDGRCE--GAKVP----SACAEGCICQPGVLSEDK- 57

Qy 60 CVP 62
Db 58 CVP 60

RBSRESULT 14
US-60-163-123-1677
; Sequence 1677, Application US/60163123
GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF

Result No.	Score	Query Match	Length	DB ID	Description
1	119	30.4	67	6 US-10-038-854-185	Sequence 185, App
2	63	16.1	60	6 US-10-039-59-59	Sequence 59, Appl
3	62.5	16.0	62	6 US-10-038-876-5	Sequence 5, Appl
4	61	15.6	66	1 PCT-US02-3277-5458	Sequence 6458, Ap
5	61	15.6	66	5 US-09-978-6458	Sequence 6458, Ap
6	61	15.6	66	6 US-10-057-438-6458	Sequence 6458, Ap
7	58.5	15.0	61	6 US-10-120-305-239	Sequence 239, App
8	58	14.8	56	1 PCT-US02-3277-9993	Sequence 9993, App
9	58	14.8	56	5 US-09-978-825-9993	Sequence 9993, App
10	58	14.8	56	6 US-10-057-458-9993	Sequence 9993, App
11	57.5	14.7	61	7 US-10-170-365-241	Sequence 241, App
12	57.5	14.7	61	7 US-60-040-068-445	Sequence 445, App
13	57	14.6	67	5 US-09-724-676-8122	Sequence 81522, A
14	57	14.6	67	5 US-09-724-81522	Sequence 81522, A
15	56.5	14.5	61	6 US-10-170-365-265	Sequence 265, App
16	56.5	14.5	61	7 US-60-423-586-136	Sequence 136, App
17	56.5	14.5	61	7 US-60-427-194-136	Sequence 136, App
18	55.5	14.2	46	5 US-09-857-815A-4	Sequence 4, Appl
19	55.5	14.2	47	5 US-09-857-815A-3	Sequence 3, Appl
20	55.5	14.2	47	5 US-09-857-815A-12	Sequence 12, Appl
21	55.5	14.2	48	5 US-09-857-815A-11	Sequence 11, Appl
22	55.5	14.2	48	5 US-09-857-815A-14	Sequence 14, Appl
23	55.5	14.2	49	5 US-09-857-815A-10	Sequence 10, Appl
24	55.5	14.2	49	5 US-09-857-815A-13	Sequence 13, Appl
25	55.5	14.2	58	6 US-10-031-778-229	Sequence 229, App
26	55.5	14.1	66	1 PCT-US02-3277-16329	Sequence 16329, A

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OM protein - protein search, using sw model

Run on: February 26, 2003, 15:11:03 ; Search Time 24 Seconds
(without alignments)
255.149 Million cell updates/sec

Title: US-09-506-978-1

Perfect score: 391

Sequence: 1 GGFGLGGRKCPNSNEIFSR.....CRLGYLRNKKVPRSKCG 67

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 486122 seqs, 91396495 residues

Total number of hits satisfying chosen parameters: 231224

Minimum DB seq length: 0
Maximum DB seq length: 67

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

LISTINGS

RESULT 1
US-10-038-854-185
; Sequence 185, Application US/10038854
; GENERAL INFORMATION:
; APPLICANT: SPYTEK, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shinkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorlina, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Paturajani, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoj, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burress, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Macdougal, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 214-02-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#	Result No.	Score	Query Match	Length	DB ID	Description
1	119	30.4	67	6 US-10-038-854-185	Sequence 185, App	
2	63	16.1	60	6 US-10-039-59-59	Sequence 59, Appl	
3	62.5	16.0	62	6 US-10-038-876-5	Sequence 5, Appl	
4	61	15.6	66	1 PCT-US02-3277-5458	Sequence 6458, Ap	
5	61	15.6	66	5 US-09-978-6458	Sequence 6458, Ap	
6	61	15.6	66	6 US-10-057-438-6458	Sequence 6458, Ap	
7	58.5	15.0	61	6 US-10-120-305-239	Sequence 239, App	
8	58	14.8	56	1 PCT-US02-3277-9993	Sequence 9993, App	
9	58	14.8	56	5 US-09-978-825-9993	Sequence 9993, App	
10	58	14.8	56	6 US-10-057-458-9993	Sequence 9993, App	
11	57.5	14.7	61	7 US-10-170-365-241	Sequence 241, App	
12	57.5	14.7	61	7 US-60-040-068-445	Sequence 445, App	
13	57	14.6	67	5 US-09-724-676-8122	Sequence 81522, A	
14	57	14.6	67	5 US-09-724-81522	Sequence 81522, A	
15	56.5	14.5	61	6 US-10-170-365-265	Sequence 265, App	
16	56.5	14.5	61	7 US-60-423-586-136	Sequence 136, App	
17	56.5	14.5	61	7 US-60-427-194-136	Sequence 136, App	
18	55.5	14.2	46	5 US-09-857-815A-4	Sequence 4, Appl	
19	55.5	14.2	47	5 US-09-857-815A-3	Sequence 3, Appl	
20	55.5	14.2	47	5 US-09-857-815A-12	Sequence 12, Appl	
21	55.5	14.2	48	5 US-09-857-815A-11	Sequence 11, Appl	
22	55.5	14.2	48	5 US-09-857-815A-14	Sequence 14, Appl	
23	55.5	14.2	49	5 US-09-857-815A-10	Sequence 10, Appl	
24	55.5	14.2	49	5 US-09-857-815A-13	Sequence 13, Appl	
25	55.5	14.2	58	6 US-10-031-778-229	Sequence 229, App	
26	55.5	14.1	66	1 PCT-US02-3277-16329	Sequence 16329, A	

PRIOR APPLICATION NUMBER: 60/283, 889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284, 447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286, 683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 185
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-038-854-185

RESULT 3
US-10-285-876-5
; Sequence 5, Application US/10285876
; GENERAL INFORMATION:
; APPLICANT: Sano, Takeshi
; Glazer, Alexander N
; CANTOR, Charles R
; TITLE OF INVENTION: Metallothionein Derivatives with
; LENGTH: 67
; NUMBER OF SEQUENCES: Biological Recognition Specificity
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/M-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10-285, 876
; FILING DATE: 01-Nov-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/780, 717
; FILING DATE: Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36, 627
; REFERENCE/DOCKET NUMBER: B91-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-7341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: Not Relevant
; TOPOLOGY: Not Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-285-876-5

Query Match 16.0%; Score 63; DB 6; Length 62;
Best Local Similarity 37.3%; Pred. No. 11;
Matches 19; Conservative 2; Mismatches 23; Indels 7; Gaps 3;

Query 1 GGPGGLLGRGKGPSNEIFSRQDGRQQFCPNNVPKPLIKICAPGCVYCRIG 51
Db 10 GGSGTCAGSCKCKECKCTS-CKKSCCCSCP----VGCAK-CAQGCVKAG 53

RESULT 4
PC-US02-32277-6458
; Sequence 6458, Application PC/TUS023277
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhattacharya, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda

PRIOR APPLICATION NUMBER: US 09/298, 531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065, 363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337, 930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102, 705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363, 630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124, 538
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 59
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-269-353-59

Query Match 16.1%; Score 63; DB 6; Length 60;
Best Local Similarity 38.1%; Pred. No. 9.7;
Matches 16; Conservative 2; Mismatches 20; Indels 4; Gaps 2;

Query 10 6KCPSENIESSCDGRCQRFCPNNVPKPLIKICAPG--VCR 49
Db 17 GKCPKNP--PRSIGTCVELCSQDSCPNTOKCCSNNGCIGHVCK 56

```

; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121_514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO: 6458
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Propioni acnes
; PCT-US02-32727-6458

Query Match 15.6% Score 61; DB 1; Length 66;
Best Local Similarity 31.8%; Pred. No. 17;
Matches 21; Conservative 6; Mismatches 27; Indels 12; Gaps 4;

QY          2 GFGGLGGKRC - --PSNLEFSRSDGRFCRCPNVPKLCKICAPGGVCRLLGRLRNKK 58
Db          7 GRELISAGKCGFRPSDQ - -RRCQAQQGRLPQSRRPVSRCVR --- -CIC -CSLRASPL 57

Qy          59 VCVPRS 64
Db          58 PCQPPS 63

RESULT 5
US-09-918-825-6458
; Sequence 6458, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Blatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Sijing
; APPLICANT: Jen, Shiyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121_514C1
; CURRENT APPLICATION NUMBER: US/09/978, 825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO: 6458

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; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 64 58
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Propioni acnes

RESULT 5
US-09-978-825-6458
; Sequence 6458, Application US/09978825
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Steiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bharia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Sining
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121_514C1
; CURRENT APPLICATION NUMBER: US/09/978, 825
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NCS: 30992
SEQ ID NO: 6458

RESULT 7
US-10-170-385-239 ; Sequence 239, Application US/10170385
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Raver, William Nigel
; APPLICANT: Taylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krieger, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532662000100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIORITY NUMBER: PCT/GB02/01662
PRIORITY FILING DATE: 2002-04-08
PRIORITY NUMBER: PCT/GB01/05458
PRIORITY FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS.: 549

RESULT 8
PC/US02-32727-9993
Sequence 9993, Application PC/TU/S02/32727
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay

```

; APPLICANT: Zhang, Yanni ; APPLICANT: Persing, David ; APPLICANT: Wang, Sining ; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; APPLICANT: Jen, Shyan ; FILE REFERENCE: 210121_5141 ; APPLICANT: Lodes, Michael ; GENERAL INFORMATION: ; FILE REFERENCE: 210121_5141
; APPLICANT: Benson, Darin ; CURRENT APPLICATION NUMBER: US/10/057,498 ; APPLICANT: Jones, Robert ; CURRENT FILING DATE: 2003-04-20
; APPLICANT: Carter, Barrick ; NUMBER OF SEQ ID NOS: 29212 ; SEQ ID NO: 9993 ; NUMBER OF SEQ ID NOS: 29212
; APPLICANT: Barth, Brenda ; LENGTH: 56 ; SEQ ID NO: 9993 ; LENGTH: 56
; APPLICANT: Douglass, John ; TYPE: PRT ; ORGANISM: Propioni acnes
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes ; FILE REFERENCE: 210121_514C1 ; SEQ ID NO: 9993 ; US-10-057-9993
; CURRENT APPLICATION NUMBER: PCT/US02/32727 ; LENGTH: 56 ; NUMBER OF SEQ ID NOS: 30952 ; NUMBER OF SEQ ID NOS: 30952
; CURRENT FILING DATE: 2002-10-11 ; SEQ ID NO: 9993 ; PCT-US02-32727-9993

Query Match 32 VVPKPLCIKICAPGCVCRGLYLRNKKVCPVR 63
Best Local Similarity 37.5%; Pred. No. 31; Score 58; DB 1; Length 56;
Matches 12; Conservative 4; Mismatches 16; Indels 0; Gaps 0;
Length 56; Score 58; DB 6; Length 56;
Organism: Propioni acnes ; Sequence 241, Application US/10170385
; GENERAL INFORMATION: ; CURRENT APPLICATION NUMBER: US/10/057,498
; APPLICANT: Ward, Neil Raymond ; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On ; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan ; APPLICANT: Binley, Katie Mary
; APPLICANT: Bayner, William Nigel ; APPLICANT: Naylors, Stuart
; APPLICANT: Kingsman, Susan Mary ; APPLICANT: Krieger, David
; APPLICANT: Skeiky, Yasir ; APPLICANT: Title of Invention: ANALYSIS METHOD
; APPLICANT: Persing, David ; FILE REFERENCE: 53:682000:100
; APPLICANT: Bhatia, Ajay ; CURRENT APPLICATION NUMBER: US/10/170,385
; APPLICANT: Maisonneuve, Jean Francois ; CURRENT FILING DATE: 2002-06-12
; APPLICANT: Zhang, Yanni ; PRIORITY NUMBER: PCT/GB02/01662
; APPLICANT: Wang, Sining ; PRIOR FILING DATE: 2002-04-08
; APPLICANT: Jen, Shyan ; PRIORITY APPLICATION NUMBER: PCT/GB01/05458
; APPLICANT: Lodes, Michael ; PRIOR FILING DATE: 2001-12-10
; APPLICANT: Benson, Darin ; NUMBER OF SEQ ID NOS: 549
; APPLICANT: Jones, Robert ; SOFTWARE: Fast-SEQ for Windows Version 4.0
; APPLICANT: Carter, Barrick ; SEQ ID NO: 241
; APPLICANT: Barth, Brenda ; LENGTH: 61
; APPLICANT: Douglass, John ; TYPE: PRT
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes ; ORGANISM: Homo Sapiens
; CURRENT APPLICATION NUMBER: US/09/978,825 ; Sequence 445, Application US/60440068
; CURRENT FILING DATE: 2003-01-29 ; RESULT 12
; NUMBER OF SEQ ID NOS: 30992 ; Best Local Similarity 32.6%; Pred. No. 37;
; SEQ ID NO: 9993 ; Matches 15; Conservative 6; Mismatches 20; Indels 5; Gaps 4;
; LENGTH: 56 ; Score 57.5%; DB 6; Length 61;
; TYPE: PRT ; Organism: Homo Sapiens ; Sequence 445, Application US/60440068
; APPLICANT: Nader, Steven G. ; APPLICANT: Carman, Julie
; APPLICANT: Mitcham, Jennifer ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHWAY
; APPLICANT: Skeiky, Yasir ; FILE REFERENCE: 3053-4191
; CURRENT APPLICATION NUMBER: US/60/440,068 ; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 7446 ; NUMBER OF SEQ ID NOS: 7446
; SOFTWARE: PatentIn Ver. 2.1 ; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO: 445
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-440-068-445

Query Match 14.7%; Score 57.5; DB 7; Length 61;
Best Local Similarity 36.7%; Pred. No. 37;
Matches 18; Conservative 2; Mismatches 22; Indels 7; Gaps 3;

Qy  1 GGGGGLGRGKCPNSNETFSRCDGRQRFPCBNVVPKPLCIRKAPGCCVR 49
Db  10 GGSCTAGSCKCKECKCTS-CKKSCCSCCP---VGAK-CAGCCK 51

RESULT 13
US-09-724-676-81522
; Sequence 81522, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 81522
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-81522

Query Match 14.6%; Score 57; DB 5; Length 67;
Best Local Similarity 43.2%; Pred. No. 45;
Matches 16; Conservative 1; Mismatches 16; Indels 4; Gaps 2;

Qy  1 GGGGGLGRGKCPNSNETFSRCDGRQRFPCPNVVPK 36
Db  16 GGGGGGGGWEKCLE--FPLAIGHSNKLCPRVSPFP 49

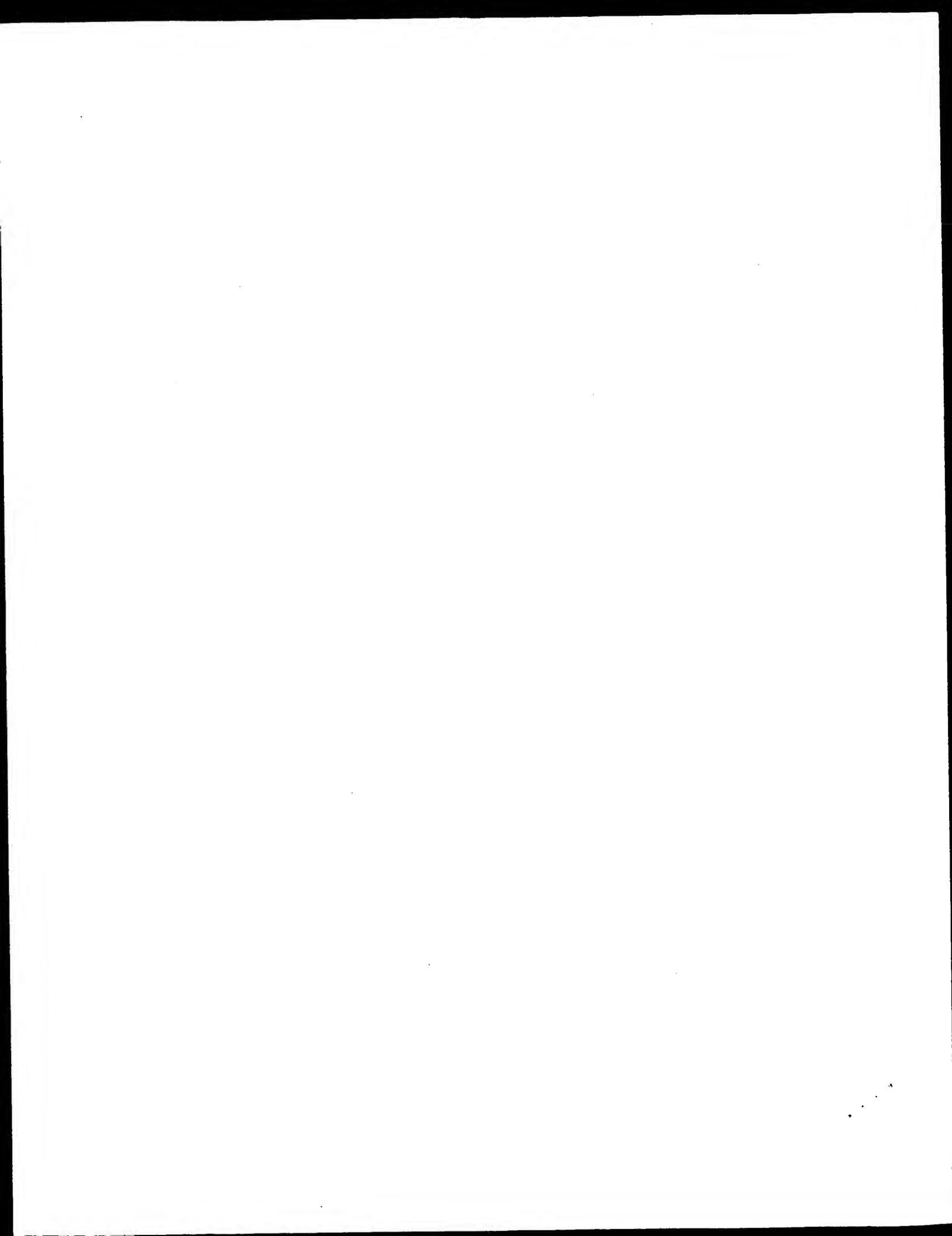
RESULT 14
US-09-724-676A-81522
; Sequence 81522, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724, 676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 81522
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-81522

Query Match 14.6%; Score 57; DB 5; Length 67;
Best Local Similarity 43.2%; Pred. No. 45;
Matches 16; Conservative 1; Mismatches 16; Indels 4; Gaps 2;

Qy  1 GGGGLGRGKCPNSNETFSRCDGRQRFPCPNVVPK 36
Db  16 GGGGGGGGWEKCLE--FPLAIGHSNKLCPRVSPFP 49

RESULT 15
US-10-170-385-265
; Sequence 265, Application US/10170385
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert

```



Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - protein search, using sw model
Run on: February 26, 2003, 15:10:07 ; Search time 14 Seconds
(without alignments)
140,810 Million cell updates/sec

Title: US-09-506-978-1
Perfect score: 391
Sequence: 1 GGFGLGGRKCPNSNEIFSR.....CRIGYLRNKKVVCPRSKCG 67

Scoring table: BLOSUM62
Gapext: 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 188167

Minimum DB seq length: 0
 Maximum DB seq length: 67

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

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 4: /cgns2_6/podata/1/1aa/6B-COMB.pep:
 5: /cgns2_6/podata/1/1aa/PCTUS_COMB.pep:
 6: /cgns2_6/podata/1/1aa/backfile1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	82	21.0	61	2 US-09-465-380-01	Sequence 61, App1
2	82	21.0	61	2 US-09-486-397-01	Sequence 61, App1
3	82	21.0	61	2 US-09-486-399-61	Sequence 61, App1
4	82	21.0	61	2 US-09-461-965-01	Sequence 61, App1
5	82	21.0	61	2 US-09-634-641-01	Sequence 61, App1
6	82	21.0	61	3 US-09-249-471-61	Sequence 61, App1
7	82	21.0	61	3 US-09-249-472-61	Sequence 61, App1
8	82	21.0	61	3 US-09-249-451-01	Sequence 61, App1
9	82	21.0	61	3 US-09-809-455-01	Sequence 61, App1
10	82	21.0	61	3 US-09-249-461-01	Sequence 61, App1
11	82	21.0	61	3 US-09-249-448-61	Sequence 61, App1
12	68	17.4	47	2 US-09-637-759B-00	Sequence 60, App1
13	68	17.4	47	3 US-09-871-355A-00	Sequence 60, App1
14	68	17.4	47	4 US-09-201-475-00	Sequence 60, App1
15	68	17.4	58	2 US-09-465-380-00	Sequence 60, App1
16	68	17.4	58	2 US-09-486-397-60	Sequence 60, App1
17	68	17.4	58	2 US-09-486-399-60	Sequence 60, App1
18	68	17.4	58	2 US-09-461-965-00	Sequence 60, App1
19	68	17.4	58	2 US-09-634-641-00	Sequence 60, App1
20	68	17.4	58	3 US-09-249-471-60	Sequence 60, App1
21	68	17.4	58	3 US-09-249-472-60	Sequence 60, App1
22	68	17.4	58	3 US-09-249-451-00	Sequence 60, App1
23	68	17.4	58	3 US-09-809-455-00	Sequence 60, App1
24	68	17.4	58	3 US-09-249-461-00	Sequence 60, App1
25	68	17.4	58	3 US-09-249-448-60	Sequence 60, App1
26	62.5	16.0	62	4 US-07-780-717C-5	Sequence 5, App1
27	59.5	15.2	61	2 US-08-785-530-03	Sequence 3, App1

ALIGNMENTS

RESULT 1
 US-09-465-380-01
 ; Sequence 61, Application US/08465380
 ; Patent No. 5863894
 ; GENERAL INFORMATION:
 ; ; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
 ; ; Joris H.L. Mensens, Marc J. Lauwers, Yves R. Laroche, Laurent S. Jespers,
 ; ; Yannick G.J. Ganssemans, Matthew Moyle,
 ; ; APPLICANT: Peter W. Bergum
 ; ; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
 ; ; NUMBER OF SEQUENCES: 356
 ; ; CORRESPONDENCE ADDRESS:
 ; ; ADDRESSE: Lyon & Lyon
 ; ; STREET: 633 West Fifth Street
 ; ; CITY: Los Angeles
 ; ; STATE: California
 ; ; COUNTRY: U.S.A.
 ; ; ZIP: 90071
 ; ; COMPUTER READABLE FORM:
 ; ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb.
 ; ; MEDIUM TYPE: Storage
 ; ; COMPUTER: IBM Compatible
 ; ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; ; SOFTWARE: Word Perfect 5.1
 ; ; CURRENT APPLICATION DATA:
 ; ; APPLICATION NUMBER: US/08/465,380
 ; ; FILING DATE: June 5, 1995
 ; ; CLASSIFICATION: 530
 ; ; PRIOR APPLICATION DATA:
 ; ; APPLICATION NUMBER: 08/326,110
 ; ; FILING DATE: October 18, 1994
 ; ; ATTORNEY/AGENT INFORMATION:
 ; ; NAME: BIGGS, SUZANNE L.
 ; ; REGISTRATION NUMBER: 30,158
 ; ; REFERENCE/DOCKET NUMBER: 211/268
 ; ; TELECOMMUNICATION INFORMATION:
 ; ; TELEPHONE: (213) 489-1600
 ; ; TELEX: 67-3510
 ; ; INFORMATION FOR SEQ ID NO: 61:
 ; ; SEQUENCE CHARACTERISTICS:
 ; ; LENGTH: 61 amino acids
 ; ; TYPE: amino acid
 ; ; TOPOLOGY: linear
 ; ; MOLECULE TYPE: peptide
 ; ; ORIGINAL SOURCE: Nector americanus
 ; ; ORGANISM: Nector americanus

US-08-465-380-61
 Query Match 21.0%; Score 82; DB 2; Length 61;
 Best Local Similarity 30.9%; Pred. No. 0.051;
 Matches 17; Conservative 9; Mismatches 19; Indels 10; Gaps 2;

Qy 12 CPSNEIFSRDGRCORFCPNNVPKPLCIRKAPGCV----CRGLYLRNKKVVCV 61
 Db 4 CPANEWRECGTCPPEPKCNQMP----DICTMNCIVDVQCCKEYKRHETKGCL 53

RESULT 2

US-08-486-397-61

Sequence 61, Application US/08486397

Patent No. 5866542

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Joris H.L. Mensens, Marc J. Lauwers,

APPLICANT: Yves R. Laroche, Laurent S. Jespers,

APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,399

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 213/270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE: Necator americanus

US-08-486-399-61

Query Match 21.0%; Score 82; DB 2; Length 61;

Best Local Similarity 30.9%; Pred. No. 0.051;

Matches 17; Conservative 9; Mismatches 19; Indels 10; Gaps 2;

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE: Necator americanus

US-08-486-397-61

RESULT 4

US-08-461-965-61

Sequence 61, Application US/08461965

Patent No. 5872098

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Joris H.L. Mensens, Marc J. Lauwers,

APPLICANT: Yves R. Laroche, Laurent S. Jespers,

APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

RESULT 3

US-08-486-399-61

Sequence 61, Application US/08486399

Patent No. 5866543

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Joris H.L. Mensens, Marc J. Lauwers,

APPLICANT: Yves R. Laroche, Laurent S. Jespers,

APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C., DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,965
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 210/243
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE: Peptid
 ORGANISM: Necator americanus
 US-08-461-965-61

Query Match 21.0%; Score 82; DB 2; Length 61;
 Best Local Similarity 30.9%; Pred. No. 0.051%; Gaps 2;

Matches 17; Conservative 9; Mismatches 19; Indels 10; Gaps 2;
 Qy 12 CPSNETFSRCDGRQRFCPNVPKPLCIIKICAPGV---CRIGYLRLNRKKVY 61
 1||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 4 CPANEWRECGTPCPFKNPMP---DICTMNCIVDVQCCKBGSYKRHETKGEL 53
 |||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 RESULT 5
 US-08-634-641-61

; Sequence 61, Application US/08634641
 ; Patent No. 5955294
 ; GENERAL INFORMATION:
 ; APPLICANT: Vlasuk, George P. Vlasuk
 ; APPLICANT: Stanssens, Patrick Eric Hugo
 ; APPLICANT: Mensens, Joris Hilda Lieven
 ; APPLICANT: Lauwers, Marc Josef
 ; APPLICANT: Larocque, Yves Rene
 ; APPLICANT: Jaspers, Laurent Stephane
 ; APPLICANT: Ganssemans, Yannick Georges Jozef
 ; APPLICANT: Moyle, Matthew
 ; APPLICANT: Bergum, Peter W.
 ; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
 ; NUMBER OF SEQUENCES: 356
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

RESULT 6
 US-09-249-471-61
 ; Sequence 61, Application US/09249471
 ; Patent No. 6040441
 ; GENERAL INFORMATION:
 ; APPLICANT: Vlasuk, George Phillip
 ; APPLICANT: Stanssens, Patrick Eric Hugo
 ; APPLICANT: Mensens, Joris Hilda Lieven
 ; APPLICANT: Lauwers, Marc Josef
 ; APPLICANT: Larocque, Yves Rene
 ; APPLICANT: Jaspers, Laurent Stephane
 ; APPLICANT: Ganssemans, Yannick Georges Jozef
 ; APPLICANT: Moyle, Matthew
 ; APPLICANT: Bergum, Peter W.
 ; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
 ; NUMBER OF SEQUENCES: 356
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/249,471
 FILING DATE:
 APPLICATION NUMBER: 08/809,455
 FILING DATE: April 17, 1997
 APPLICATION NUMBER: PCT/US95/13231
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 216/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE: Neator americanus
 US-09-249-471-61

Query Match 21.0%; Score 82; DB 3; Length 61;
 Best Local Similarity 30.3%; Pred. No. 0.05%; Indels 10; Gaps 2;
 Matches 17; Conservative 9; Mismatches 19; Indels 10; Gaps 2;

Qy 12 CPSNEIFSRCDGRCORFCPQVVKPKLICIKTAPGV----CRLGYLRNKKVYKV
 Db 4 CPANEERCGTCPCEPKCNQMP----DICTMNCIVDVQCCKEGYKRHETKGCL 53

RESULT 7
 Sequence 61, Application US/09249472
 Patent No: 606318
 GENERAL INFORMATION:
 APPLICANT: Vlaasuk, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwerys, Marc Joseph
 APPLICANT: La Roche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gansmans, Yannick Georges Jozef
 APPLICANT: Moyle, Matthew
 APPLICANT: Bergum, Peter W.
 TITLE OF INVENTION: NEMATO-E-XTRACTED SERINE PROTEASE
 TITLE OF INVENTION: PROTEIN INHIBITORS AND ANTICOAGULANT
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/249,472
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/809,455
 FILING DATE: April 17, 1997
 APPLICATION NUMBER: PCT/US95/13231
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 216/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 US-09-249-472-61

Query Match 21.0%; Score 82; DB 3; Length 61;
 Best Local Similarity 30.9%; Pred. No. 0.051%; Mismatches 19; Indels 10; Gaps 2;

Qy 12 CPSNEIFSRCDGRCORFCPQVVKPKLICIKTAPGV----CRLGYLRNKKVYKV
 Db 4 CPANEERCGTCPCEPKCNQMP----DICTMNCIVDVQCCKEGYKRHETKGCL 53

RESULT 8
 Sequence 61, Application US/09249451
 Patent No: 6087487
 GENERAL INFORMATION:
 APPLICANT: Vlaasuk, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwerys, Marc Joseph
 APPLICANT: La Roche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gansmans, Yannick Georges Jozef
 APPLICANT: Moyle, Matthew
 APPLICANT: Bergum, Peter W.
 TITLE OF INVENTION: NEMATO-E-XTRACTED SERINE PROTEASE
 TITLE OF INVENTION: PROTEIN INHIBITORS AND ANTICOAGULANT
 TITLE OF INVENTION: INHIBITORS AND ANTIORGULANT

TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C., DOS 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/249,451
 FILING DATE:
 PRIORITY APPLICATION NUMBER:
 APPLICATION NUMBER: 08/809,455
 FILING DATE: April 17, 1997
 APPLICATION NUMBER: PCT/US95/13231
 FILING DATE: October 17, 1995
 COMPUTER READABLE FORM:
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C., DOS 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 216/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE: Necator americanus
 US-09-249-451-61

Query Match 21 0%; Score 82; DB 3; Length 61;
 Best Local Similarity 30.9%; Pred No. 0.05%; Gaps 2;

Matches 17; Conservative 9; Mismatches 19; Indels 10; Gaps

Qy 12 CPSNEIFSRCDGRCQRFCPNVVKPLCIRKAPGVY---CRUGYLRLNKKKVCV 61
 Db 4 CPANEWRECGTPEPKCQMP---DICTMNCIVDVQCQREGYKRHETRKGCL 53

RESULT 9
 us-09-455-61
 Sequence 61. Application US/08809455
 Patent No. 6090916
 GENERAL INFORMATION:
 APPLICANT: Vlasuk, George Phillip
 APPLICANT: Scansens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwers, Marc Josef
 APPLICANT: Laroche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Ganssemans, Yannick Georges Jozef

APPLICANT: Moyle, Matthew
 APPLICANT: Bergum, Peter W.
 TITLE OF INVENTION: NEURATODE EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT
 TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C., DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,455
 FILING DATE: April 17, 1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13231
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 216/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Necator americanus
 US-08-809-455-61

RESULT 10
 US-09-249-461-61
 Sequence 61. Application US/09249461
 Patent No. 6096577
 GENERAL INFORMATION:
 APPLICANT: Vlasuk, George Phillip
 APPLICANT: Stansens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwers, Marc Josef
 APPLICANT: Laroche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Ganssemans, Yannick Georges Jozef

; APPLICANT: Jaspers, Laurent Stephane
 ; APPLICANT: Ganssmans, Yannick Georges Jozef
 ; APPLICANT: Moyle, Matthew Peter W.
 ; APPLICANT: Bergum, Peter W.
 ; TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE
 ; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 356
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; SUITE: 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: Storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/249,461
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/809,455
 ; FILING DATE: April 17, 1997
 ; APPLICATION NUMBER: PCT/US95/13231
 ; FILING DATE: October 17, 1995
 ; APPLICATION NUMBER: 08/486,399
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/486,397
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/465,380
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/461,965
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/326,110
 ; FILING DATE: October 18, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BIGGS, SUZANNE L.
 ; REGISTRATION NUMBER: 30,158
 ; REFERENCE/DOCKET NUMBER: 216/270
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 61:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 61 amino acids
 ; TYPE: amino acids
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE: Necator americanus
 ; ORGANISM: Necator americanus
 ;
 US-09-249-461-61

Query Match 21.0% Score 82; DB 3; Length 61;
 Best Local Similarity 30.9%; Pred. No. 0.051; Gaps 2;
 Matches 17; Conservative 9; Mismatches 19; Indels 10; Gaps 2;
 US-09-249-448-61

RESULT 11
 US-09-249-448-61
 ; Sequence 61, Application US/09249448
 ; Patent No. 612435
 ; GENERAL INFORMATION:
 ; APPLICANT: Vlasuk, George Phillip

; APPLICANT: Staussens, Patrick Eric Hugo
 ; APPLICANT: Messens, Joris Hilda Lieven
 ; APPLICANT: Lauvereys, Marc Josef
 ; APPLICANT: Laroche, Yves Rene
 ; APPLICANT: Jespers, Laurent Stephane
 ; APPLICANT: Ganssmans, Yannick Georges Jozef
 ; APPLICANT: Moyle, Matthew Peter W.
 ; APPLICANT: Bergum, Peter W.
 ; TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE
 ; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
 ; NUMBER OF SEQUENCES: 356
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; SUITE: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/249,448
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/809,455
 ; FILING DATE: April 17, 1997
 ; APPLICATION NUMBER: PCT/US95/13231
 ; FILING DATE: October 17, 1995
 ; APPLICATION NUMBER: 08/486,399
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/486,397
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/465,380
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/461,965
 ; FILING DATE: June 5, 1995
 ; APPLICATION NUMBER: 08/326,110
 ; FILING DATE: October 18, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BIGGS, SUZANNE L.
 ; REGISTRATION NUMBER: 30,158
 ; REFERENCE/DOCKET NUMBER: 216/270
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 61:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 61 amino acids
 ; TYPE: amino acids
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE: Necator americanus
 ; ORGANISM: Necator americanus
 ;
 US-09-249-448-61

Query Match 21.0% Score 82; DB 3; Length 61;
 Best Local Similarity 30.9%; Pred. No. 0.051; Gaps 2;
 Matches 17; Conservative 9; Mismatches 19; Indels 10; Gaps 2;
 US-09-249-448-61

Qy 12 CPSNETSRCDGRCORFCPNVVPKPLCIKICAPGCV----CRIGYLRLNKKVGV 61
 Db 4 CPANEEMRECGTPCEPKCNQMP---DICTMMNC1IVDVCOCKEGYKRHETKGCL 53

RESULT 12
 US-09-249-448-61
 ; Sequence 61, Application US/09249448
 ; Patent No. 612435
 ; GENERAL INFORMATION:
 ; APPLICANT: Vlasuk, George Phillip

RESULT 12
 US-08-637-759B-400

Sequence 400, Application US/08637759B
 ; GENERAL INFORMATION:
 ; APPLICANT: David William Holden
 ; TITLE OF INVENTION: Identification of Genes
 ; NUMBER OF SEQUENCES: 501
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: USA
 ; ZIP: 30309-3450
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/637-759B
 ; FILING DATE: 03-MAY-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB95/02875
 ; FILING DATE: 11-DEC-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31-284
 ; REFERENCE/DOCKET NUMBER: RPMS 101 CON
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404) 873-8794
 ; TELEFAX: (404) 873-8795
 ; INFORMATION FOR SEQ ID NO: 400:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 47 amino acids
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; US-08-637-759B-400

Query Match 17.4%; Score 68; DB 2; Length 47;
 Best Local Similarity 55.6%; Pred. No. 1.1;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

RESULT 13
 US-08-871-355A-400
 Sequence 400, Application US/08871355A
 ; GENERAL INFORMATION:
 ; APPLICANT: David William Holden
 ; TITLE OF INVENTION: Identification of Genes
 ; NUMBER OF SEQUENCES: 501
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: USA
 ; ZIP: 30309-3450
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31-284
 ; REFERENCE/DOCKET NUMBER: RPMS 101 CON
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404) 873-8794
 ; TELEFAX: (404) 873-8795
 ; INFORMATION FOR SEQ ID NO: 400:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 47 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: No
 US-09-201-945-400

Query Match Score 17.4%; Pred. No. 1.1;
 Best Local Similarity 55.6%; Mismatches 2; Length 47;
 Matches 10; Conservative 10; Indels 0; Gaps 0;
 Qy 12 OPSNEIFSRCGRCDGRFC 29
 ||| : | | | | | | | | | | | |
 Db 30 CPAGRPLSRCDGRCDIEC 47

RESULT 15
 US-08-465-380-60
 ; Sequence 60, Application US/08465380
 ; Patent No. 5863894
 ; GENERAL INFORMATION:
 ; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
 ; APPLICANT: Joris H.L. Mensens, Marc J. Lauwers,
 ; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
 ; APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,
 ; APPLICANT: Peter W. Bergum
 ; TITLE OF INVENTION: NEUTRODE-EXTRACTED ANTICOAGULANT
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 356
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C., DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/465,380
 ; FILING DATE: June 5, 1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/326,110
 ; FILING DATE: October 18, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BIGGS, SUZANNE L.
 ; REGISTRATION NUMBER: 30,158
 ; REFERENCE/DOCKET NUMBER: 213/268
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 60:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 58 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE: Heligmosomoides polygyrus
 ; ORGANISM: Heligmosomoides polygyrus

Qy 12 CPSNEIFSRCGRCDGRFC 29
 ||| : | | | | | | | | | | | |
 Db 3 CGPNEEETECGTPCEPKNEPMAPDICTLNCTVNVCOCKPGKRGPKGVAPGPGC 57

Search completed: February 26, 2003, 15:13:22
 Job time : 15 secs